Boselaphu Boselaphu

Cervus un

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AY456907 AY456905 AY456906

AY286441 AY456905 AY456906 AY456907 AY456907

Cervus un

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AY286429 A AY286431 A AY286438 B AY286440 B AY286441 B

Antilope

AY286436 AY286434 AY286435

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AY286429 AY286431 AY286438

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Perdicula Lepidoche Lepidoche Brachyram Brachyram Brachyram Brachyram

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AY540848 AY286430 AY390778 B

Axis

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AY390776 AF433207 AF306868

AF306869 AF306870 AF306871 AF306872

AY286430 AY390778 AY390775

AY540848 AY540847

AY390776 I AF433207 C AF306868 E AF306869 E AF306870 E AF306871 E

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/noTe="Universal primer for amplifying a fragment of cytochrome b gene of animal species in polymerase chain
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AF459430
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1 Similarity 100.0%; Score 25; DB 6; Length 25;
25; Conservative 0; Mismatchor
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Universal primers for wildlife identification
Patent: WO 02077278-A 2 03-OCT-2002;
Council of Scientific and Industrial Research (IN)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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Sequence 2 from Patent W002077278.
AX565561
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synthetic construct
artificial sequences.
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U18258 Spharagemon
U18253 Trimerotrop
AF371961 Bos tauru
S49215 apocytochro
AY217671 Xenopus 1
AY217686 Xenopus 1
AY217680 Xenopus 1
AY217691 Xenopus 1
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AY004180 Parapodis
AY004205 Primnoa 1
U17904 Circotettix
U18250 Camnula pel
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AF145511 Melanoplu
AF145531 Melanoplu
                                                                                                   November 16, 2004, 22:33:39; Search time 136.759 Seconds (without alignments) 8644.709 Million cell updates/sec
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Compugen Ltd.
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Copyright (c) 1993 - 2004
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Gaps

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Melanoplus foedus
                                                                                                                                                                                                                                                         169 TACCATGAGGACAAATATCATTCTG 193
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Matches 25; Conservative
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                  Engraulis encrasicolus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Meopterygii, Teleostei, Clupeomorpha, Clupeiformes,
Engraulidae, Engraulis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ^protein_id="AAL78336.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF145511 258 bp DNA linear INV 17-DEC-2001 Melanoplus angustipennis cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product.
AF145511 GI:5918571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               grasshopper)
Melanoplus angustipennis
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera, Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Melanoplinae; Melanoplus.

(bases 1 to 258)
Molecular phylogeny of melanopline grasshoppers (Orthoptera: Acrididae). The genus Melanopline
                                                                                                                                Direct Submission
Submitted (17-DEC-2001) Genetica, Universidad de Vigo, Campus
Lagoas Marcosende, Vigo 36200, Spain
Location/Qualifiers
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mitochondrion Engraulis encrasicolus (European anchovy)
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                                                                                                                                                                                                                               /organism="Engraulis encrasicolus"
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/transl_table=2
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LVmatafmgyvLpwggmsfwgatvitnilsaipylgtblvg"
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Barytettix humphreysi cytochrome b gene, partial cds; mitochondrial
gene for mitochondrial product.
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Melanoplus foedus cytochrome b gene, partial cds, mitochondrial
gene_for mitochondrial product.
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Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Acridoidae, Melanoplinae; Melanoplus.
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Molecular phylogeny of melanopline grasshoppers (Orthoptera: Acrididae). The genus Melanoplus
Ann. Entowol. Soc. Am. 92 (5), 617-623 (1999)
2. (bases 1 to 258)
Chapco, W., Kuperus, W.R. and Litzenberger, G.S.
Direct Submission
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Gaps

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Prince Involved 1558 bp DNA linear INV 04-MAY-2002 gene for mitochondrial product.
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LymatafmgyvlpwgqmsfwgatvitwllsaipYlgmblvQ"
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Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Catantopinae; Primnoa.

E 1 (bases 1 to 258)
S Litzanberger, G. and Chapco, W.
Molecular Phylogeny of Selected Eurasian Podismine Grasshoppers
(Orthoptera: Acrididae)
L Ann. Entomol. Soc. Am. 94 (4), 505-511 (2001)
E 2 (bases 1 to 258)
Litzanberger, G.s. and Chapco, W.
S Litzanberger, G.s. and Chapco, W.
Direct Submission
L Submitted (04-UUI-2000) Biology, University of Regina, 3737 Wascana Parkway, Regina, Saskatchewan 548 0A2, Canada
Location/Qualifiers
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Circotettix carlinianus mitochondrion cytochrome b gene, partial
cds.
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/country="Russia"
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/organism="Primnoa litoralis"
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CCU17904
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AY004205
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Ann. Bntomol. Soc. Am. 94 (4), 505-511 (2001)
2 (bases 1 to 258)
Litzenberger, G.S. and Chapco, W.
Direct Submission
Submitted (04-UUL-2000) Biology, University of Regina, 3737 Wascana Parkway, Regina, Saskatchewan S4S 0A2, Canada
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0
                                                                Barytettix humbreysi

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteracidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Melanoplinae; Barytettix.

1 (bases 1 to 258)
Litzenberger, G.S. and Chapco, W.

Direct Submission

Submitted (26-OCT-2000) Department of Biology, University of Regina, 3737 Wascana Parkway, Regina, Saskatchewan S4S 0A2, Canada Location/Qualifiers
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Acrididae, Catantopinae, Parapodisma.
1 (bases 1 to 258)
Litzenberger, G. and Chapco, W.
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/note="obtained from dried hind femur"
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/organelle="mitochondrion"
                                                mitochondrion Barytettix humphreysi
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/codon_start=3
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        AF317194.1 GI:33337314
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INV 13-DEC-1994

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/db_xref="G1:624168"
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LVMATAFNGYVLPWGQMSFWGATVITNLLSAIPYIGTDIVQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCU18257 27-JAN-1995 Spharagemon collare cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds.
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1 (bases 1 to 258)
Chapco, W. and Martel, R.K.B.
Mitochondrial DNA sequence variation in North American band-winged
                                                                                                                                                                                                                                                                                                                                       Gaps
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/dev_stage="adult"
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|dev_stage="adult"
      /mol_type="genomic_DNA"
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/db_xref="taxon:37261"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Spharagemon collare"
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/transl_table=5
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2 (bases 1 to 258)
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Best Local Similarity
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protein id="AAA5113.1"
db xref="G1:601797"
/translation="IIRTFHANGASMFFICIYLHVGRGIYYGSYMYMNTGTVILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPUI8250
Campula pellucida cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds.
                                                    mitochondrion Aerochoreutes carlinianus
Aerochoreutes carlinianus
Necotoreutes carlinianus
Necotoreutes carlinianus
Necotoreutes (Arthoropoda, Hexapoda, Insecta, Pterygota,
Necotore, Orthopteroidea, Orthoptera; Caelifera; Acridomorpha,
Acridoidea, Acrididae, Oedipodinae, Aerochoreutes.

( Gases I to 258)

( Chapco, W. and Martel, R.K. B.
Mitochondrial DNA sequence variation in North American hand-winged
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Camnula pellucida
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Camnula.
Chases I to 2581
Chapco, W. and Martel, R.K.B.
Mitochondrial DNA sequence variation in North American band-winged
                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-DEC-1994) Chapco W., University of Regina, Biology,
Regina, Saskatchewan, Canada, S4S 0A2
Location/Qualifiers
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Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, 848 0A2, Canada
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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/tissue_type="whole organism minus gut"
/dev_stage="adult"
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/organelle="mitochondrion"
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/organelle="mitochondrion"
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transI table=5
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2 (bases 1 to 258)
                    U17904.1 GI:601796
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Best Local Similarity
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LVmatafmgyvLpwGQmsFwGaTVITnkLsAiPYmGTEIVQ"
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mitochondrial gene
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Mitochondrial DNA sequence variation in North American band-winged
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Mitochondrial DNA sequence variation in North American band-winged
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                                                                                                                                                                                            Spharagemon campestris
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acridoidea; Oedipodinae; Spharagemon.
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Trimerotropis pistrinaria
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acridiae; Oedipodinae; Trimerotropis.
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Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S DA2, Canada
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organelle="mitochondrion"
|mol_type="genomic DNA"
'isolate="Last Mountain Lake, Saskatchewan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 3; Length 258; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole organism minus gut"
/dev_stage="adult"
                                                                    SCU18258 258 bp DNA 1 Spharagemon campestris cytochrome b gene, miencoding mitochondrial protein, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Spharagemon campestris"
                                                                                                                                                                            mitochondrion Spharagemon campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA61679.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
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2 (bases 1 to 258)
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Unpublished
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Best Local Similarity
Matches 25; Conserv
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SCU18258
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279 bp DNA linear MAM 22-FEB-2002 Bos taurus cytochrome b (cytb) gene, partial cds; mitochondrial AF371961
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/protein id="AAK53817.1"
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/translation="SIRTLHAYGASMFFICIYLHVGRGIYYGSYMYMNTWMTGTMILF
LVMATAFMGYVLPWGQMSFWGATVIYNLLSAIPYMGTEIVQ"
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Bottero,M.T. and Rosati,S.
Boirect Submission
Submitted (18-APR-2011) Produzioni Animali, Facolta' di Medicina
Veterinaria, Via Nizza, 52, Torino, TO 10126, Italy
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bottero, M.T., Civera, T., Anastasio, A., Turi, R.M. and Rosati, S. Identification of cow's milk in 'buffalo' cheese by duplex polymerase chain reaction
J. Food Prot. 65 (2), 362-366 (2002)
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Direct Submission
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
Location/Qualifiers
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/mol type="genomic DNA"
/isolate="Dilke, Saskatchewan"
/db rref="taxon:37254"
/tissue_type="whole organism minus gut"
/dev_stage="adult"
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/mol type="genomic DNA"
/db_xref="taxon:9913"
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/codon start=3
/transI table=5
/product="cytochrome b"
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/organism="Bos taurus"
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                                                                                                                   Measey,J.
Direct Submission
Submitted (11-JAN-2003) Dept. Zoology, University of the Western Submitted (11-JAN-2003) Bept. Zoology, South Africa Cape, Private Bag XI7, Bellville 7535, South Africa Location/Qualifiers
1. 290
/organism="Xenopus laevis"
                                                         Phylogeography of the genus Xenopus in southern Africa Amphib-reptil. (2003) In press 2 (bases 1 to 290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 25; DB 5; Length 290; Best Local Similarity 100.0%; Pred. No. 0.18; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 TACCATGAGGACAAATATCATTCTG 286
      Xenopodinae, Xenopus, Xenopus.
1 (bases 1 to 290)
Measey,J. and Channing,A.
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Xenopus laevis isolate 3 from South Africa cytochrome b (cytb)
mRNA, partial cds; mitochondrial gene for mitochondrial product.
AY217671
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1. (bases 1 to 279)

1. (bases 1 to 279)

1. (bases 1 to 270)

2. (box of the chit, W., Dzapo, V. and Wassmuth, R. (box of the mitochondrial DNA: restriction enzyme analysis, mapping and sequencing data
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI glabbsq 117456] from the original journal article.
Location/Qualifiers
1. .279
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93073120
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Gaps 0;

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states."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bd1g. 200 Rm 2A, Beltsville, MD 20705, USA
TTel: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
single pass sequencing. Bases called by cross_match with the -minscore 18
and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of borners gland EST and functional annotation of the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002) 22135956
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Cetartiodactyla; Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 132)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
                                                                                                                                                                                                                                                                                              3E487586 132 bp mRNA linear 176420 BARC 5BOV Bos taurus cDNA 5', mRNA sequence
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CO000322
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BP1026903
BP1026903
CR7833106
BP109501
                                                                                                                                                                                                             BM436122
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FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria;
                            Bos taurus (cow)
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CR383176 CR383176
CB227362 1RU38B07
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CB227362 1RU38B07
CB221363 1DU005F04
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ER48758 176419 BA
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Maximum Match 100%
Listing first 45 summaries
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UMC-bcl_0 RT20B09.B AU277856

UMC-bcl 0 UMC-bend UMC-bcl 0

1RT03H11

CN654069

C0000574 CK730086 UMC-bend 1Ru30F09 UMC-bend

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BP109501

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BM436122

CR383176/c LOCUS

RESULT 2

Dp

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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L (Dases I to 188)
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
10 Agri/For, Dept of AFNS, U of A, Edmonton, AB, TGG 2P5, Canada
Tel: 780 492 20169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 188 Std Error: 0.00
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Hansen, C., Fut, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gordon, P.M.K. and Moore, S.S.
Gordon, P.M.K. and Moore, S.S.
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of ArNS, University of Alberta
410 Agriffor, Dept of ArNS, U of A, Edmonton, AB, T6G 2PS, Canada
Tel: 780 492 4265
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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1Ru38B07 Bos taurus Rumen #1 library Bos taurus CDNA, mRNA
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Bos taurus
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Matches 25; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENAE, a French Animal Genome project
Unpublished (2004)
Contact: Martin P
INRA, Genomique & Physiologie de la Lactation
Domaine de Vilvert, 78852 JOUY-EN-JOSAS cedex, FRANCE
Tel: +33 (0) 1.34.65.25.82
Fax: +33 (0) 1.34.65.25.82
Email: Patrice.Martingolouy.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="bcas0003a.f.03"
/tissue type="muscles : heart, longissimus thoracis, semitendinosus, masseter cutaneus trunci"
semitendinosus, masseter cutaneus trunci"
semitendinosus, masseter cutaneus trunci"
/clone_lib="Bovine multi-stage muscles library (bcas)"
/note="Clone distribution : AGENAE Resource centre.
Francois PIUMI, Francois.Piumiajoluy,inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78322, Jouy-en-Jossas cedex, FRANCE, +33 (0)
1.34.65.28.02, +33 (0) 1.34.65.22.73"
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                                           93.8%; Score 24.4; DB 2; Length 132; 96.2%; Pred. No. 1; ive 0; Mismatches 1; Indels
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                                                                                                                                                                       61 CCTCCTAGTTTGTTGGGGATTGATCG 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
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Chevalet, C.
                                                                                           Conservative
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CB226256/c
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FEATURES

DEFINITION

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Matches

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Gaps

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/dev_erage="Day 14 pregnant" (Clone lib="POR14" (Day 14 pregnant ovine endometrium)" (Clone lib="POR14" (Day 14 pregnant covine endometrium)" (Incte="Organ: uterus; Vector: Triplex2; Site 1: EcoNI; Site 2: XhoI; Non-normalized library, sequenced 5' with Triplex2 primer (CTCCGAGATCTGGACGAGC). Library constructed by Clontech with total RNA extracted using the Trizol method and pooled from 5 females."
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Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt " -trim_fasta. Vector identified
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
                                                                                                                                                                                                                                                                                         Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&W University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
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Gray, C.A., Adelson, D.L. and Spencer, T.E. Ovine ESTs
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9940"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tspencer@ansc.tamu.edu.
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              CD288296
CD288296.1 GI:31086339
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Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 9798454896
Fax: 9798622662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 3015048414
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CK959074
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3 P21.abd POE14 (Day_14_pregnant_ovine_endometrium) Ovis aries
cDNA, mRNA sequence.
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Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Debt of AFNS, University of Alberta
10 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
/tissue_type="Stratified squamous epithelial"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab host="XL1-BlueMRF'strain"
/clone_lib="Bos taurus Rumen #1 library"
/note="Organ: Rumen; Vector: Uni-2ZAPXR; Site_1: BcoRI; Site_2: Xho I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"

/db_xref="texon:9913"

/db_xref="texon:9913"

/tissue type="Smooth muscle"

/cell_type="Simple columnar epithelial"

/dev_stage="Young adult"

/dab_host="XLI-BlueWRP'strain"

/clone_lib="Bos taurus Duodenum #1 library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Site 1: EcoRI; Site 2: Xho I'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: stephen.moore@ualberta.ca
Insert Length: 256 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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/organism="Bos taurus"
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FEATURES

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BM434895 31-JAN-2002
1RT15D07 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doubler's Bos.

1 (bases 1 to 322)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,

Bordon, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)

Unpublished (2002)

Dontact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta

10 Agriffor, Dept of AFNS, U of A, Edmonton, AB, TGG 2PS, Canada

Tel: 780 492 0169

Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
Bos taurus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/mol type="manka"
/db zref="raxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Straified squamous epithelial"
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/clone_lib="Bos taurus Reticulum #1 library"
/note="Young adult"
/clone_lib="Bos taurus Reticulum; Vector: Uni-2ZAPXR; Site_1:
EcoRI; Site_2: Xho I"
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                           Length 304;
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                                                                   1; Indels
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           93.8%; Sco...
96.2%; Pred. No. 1.-.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: stephen.moore@ualberta.ca
Insert Length: 322 Std Error: C
POLYA=No.
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                                                                                                                                    50 CCTCCTAGTTTGTTGGGGATTGATCG 25
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                      Query Match
Best Local Similarity 96.2°
Matches 25; Conservative
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Bos taurus
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1RT11H08 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
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                                                                                                                                                                                                                                                       /tissue_type="Pooled"
/dev_stage="Multiple"
/dab_host="DHLOB TI phage resistant"
/clone lib="BARC 10BDV"
/note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
BCORV; Site_2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hansen, C., Fu, A., Meng, Y., Li, C., Okine, B., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory of Alberta
Dept of AFNS, University of Alberta
Tel: 780 492 1059
Pex: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
1 (bases 1 to 304)
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/cell_type="Stratified squamous epithelial"
/cell_type="Stratified squamous epithelial"
/lab_host="Yung adult"
/lab_host="Xul-BlueMRP'strain"
/clone_lib="Ross taurus Reticulum #1 libzary"
/note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site_1:
EcoRI; Site_2: Xho I"
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by cross_match using options -minmatch 12 -minscore 12 Plate: 6 row: A column: 24 Seq primer: AGGGGATAACTATTTCACACAGG High quality sequence stop: 300.

Location/Qualifiers
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Insert Length: 304 Std Error: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCTCCTAGTTTGTTAGGGATTGATCG 26
                                                                                                                                  organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                               db_xref="taxon:9913"
clone="10BOV6_A24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                    /mol_type="mRNA"
/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM434693.1 GI:18456415
                                                                                                                                                                                                                                          sex="Male"
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Best Local Similarity
-ham 25; Conserve
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VERSION
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JOURNAL
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RESULT 8

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FEATURES

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Gaps

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BM435757 31-JAN-2002
IRu3C3.abl Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
                                                               /organism="Bos taurus"
/mol_type="mRNA"
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/db_xref="taxon:9913"
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/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: Smal; Single pass sequencing. Normalised library
constructed from bovine ovary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laborators
Dept of AFNS, University of Alberta
All Agriffor, Dept of AFNS, U of A, Edmonton, AB, T6G 2PS, Canada
Tel: 780 492 0169
Fax: 780 492 4265
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Bos taurus Rumen #1 library"
/note="Organ: Rumen; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"
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/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                            Length 328;
                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: stephen.moore@ualberta.ca
Insert Length: 330 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                              Score 24.4; Di
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                        Location/Qualifiers
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BM435757.1 GI:18457479
                                                                                                                                                                                                                                                                                                                                93.8%;
96.2%;
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1 (bases 1 to 330)
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Bos taurus
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Matches 25; Conserv
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Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Compublished (2004)
Contact: Anderson SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Sitel: EcoRI R. Site2: Smal 5' Seq Primer T3 Normalised library constructed from Deovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
Exa: 402 762 4390
Exail: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.3890904.s. Vector identified by cross_match with the -minscore 18
pCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ693580 AJ693580 taurus cDNA clone KN261-041_K22, mRNA sequence.
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Haeton, M.V., Laegreld, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.8%; Score 24.4; DB 4; Length 324; 96.2%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCTCCTAGTTTGTTAGGGATTGATCG 26
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/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone lib="MARC 4BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 137 row: P column: 3
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                           Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
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Matches 25; Conserv
                                                                                                                                                                                                                     11282978
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AJ693580/c
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TITLE
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PUBMED
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       AUTHORS
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SOURCE
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                                                                          CK727400 330 bp mRNA linear EST 23-FEB-2004 UMC-bend_0A01-006-d11 Day 5 Uterus bend Bos taurus CDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Iberia, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            blastocyst and nuclear transfer blastocyst), in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); and andometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be then of the collected can be better the following URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Helifers for the project were purchased from Circle A Ranch, Iberia, (http://www.circlearanch.com/home.html). These helfers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://genome.rnet.missouri.edu/Bovine/Methods.html.
Library construction (Standard Protocol): All procedures
have been described in detail elsewhere (Soares et al.,
1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
cellular RNA from each sample was isolated by using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 330)
Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C., Roberts, R.M., Smith, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
Contact: DNA Core Facility
Animal Science - RS Prather
University of Missouri-Columbia
MG16 Medical Sciences Bldg., Columbia, MO 65212, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: (573)884-5552
Email: bovine@rnet.missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Bog taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                           CK727400.1 GI:42580914
                                                                                                                                                                                                                                                                                                          taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                             Bos taurus
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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RESULT 13
CK727400
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Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies). The cDNAs derived from cach developmental stage of a particular tissue were selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equinolar basis and ligated directionally into the Notl and SalI sites of the pCNA-SPORTG vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH108 bacteria. Library Construction (PCR Protocol): The amount of kRNA that was recovered from cocytes and embryos was quite limiting and standard protocol. Therefore, PCR-based protocol was recovered from cocytes and embryos was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which among transcribed with a NotI-tag-dTH3 oligonucleotide and embryos). Poly-A RNA was isolated by using the Micropoly (A) Pure kit from Ambon (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dTH3 oligonucleotide and a SMART oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified oby using Chrome Spin-100 columns (1907) and polymerase (Stratagene). The resulting PCR products were fractionated by using Chrome Spin-100 columns (1907) spontal RNA contaminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96 -well plates) to confirm library quality (e.g. the presence of short polya+ tails genomic DNA contamination (must be <14,), tibosomal RNA columns and by sequencing (-4 96 -well plates) to confirm library genomic DNA contamination (must be <14,), tibosomal RNA columns of the libraries, equal NA contamination (must be < BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing CDNA libraries with fewer clones that contain long poly (dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library were pooled to produce a single mixed library (mega-library) for more extensive sequencing.
Bioinformatics work was performed by GK Springer's bioinformatics group (spoilen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Bonaldo MF, Lennon G, Soares MB, Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1966; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion library. Proc Natl Acad Sci, 91:9228-9232 TAG_TISSUE=Day 5 Uterus TAG SEQ=ATAAGATAAC"

ORIGIN

Gaps ., 93.8%; Score 24.4; DB 7; Length 330; 96.2%; Pred. No. 1.1; ive 0; Mismatches 1; Indels (1; Conservative Query Match Best Local Similarity Matches 25; Conserv

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1 CCTCCTAGTTTGTTAGGGATTGATCG 26

276 CCTCCTAGTTTGTTGGGGATTGATCG 301

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POLYA=Yes.
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  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DHJD8"
/clone_lib="BARC_5BOV"
/note="Vector: pCNV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made_from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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UMC-bcl 0A02-003-e08 Day 16 Corpus luteum from a pregnant animal bcl Bos taurus cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                      EST 27-MAR-2003
                                                                                                                                                                                                                                     1 (bases 1 to 331)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,
                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                    BE487585 331 bp mRNA linear 176419 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8414
Fax: 301 504 8414
                                                                                                                                                                                                                                                                                                                                            the bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 138 row: M column: 9 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tads@lpsi.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                       BE487585.1 GI:9607118
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                                                                                                                                                         taurus
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CN998120
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Roberts R.W. Smith, M.F. and Youngsquist, R.S.

URDA GATH NOI 2002-01976; Bovins STE: Focus on Female Reproduction

Occasiant NOI 2002/

Animal Science - RS Prather

Unpublished (2002)

Animal Science - RS Prather

Mischael Science - RS Prather

Li 3710 Massouri-Columbia, MO 65212, USA

Animal Science - RS Prather

Mischael Science - RS Prather

Li 3710 Massouri-Columbia, MO 65212, USA

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MRIG Massouri-Columbia
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was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (Occytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a Not1-tag-dT18 oligonucleotide and a SMART oligonucleotide and a SMART oligonucleotide. Sequence complementary to the SMART oligonucleotides were used swithin the SMART and dT oligonucleotides were used swithin the SMART and dT oligonucleotides were used sprimers to amplify the cDNA8 by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with Not1 and Sall and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCNV-SPORTG vector. Preliminary Library Characterization: Randomly chosen clones from each library est analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), ribosomal RNA clones (must be <1%), ribosomal RNA clones (must be <1%), ribosomal plates; of his presenting the predominant clones in each libraries, equal numbers of recombinants from each library. The clones were sequenced at the University of the libraries. library were pooled to produce a single mixed library (mega-library) for more extensive sequencing.

Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Bonaldo MF, Lennon G, Soares MB, Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jana H, Bivens NJ, Riess JE, Whitworth KM, Green JA, Porrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing CONA libraries with fewer clones that contain long poly (dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized CDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG TISSUE-Day 16 Corpus luteum from a pregnant animal

ORIGIN

0; Gaps ch 1 Similarity 96.2%; Pred. No. 1.1; 25; Conservative 0; Mismatches 1. 1727) Query Match Best Local Similarity Matches 25; Conserv

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1 CCTCCTAGITIGITAGGGATIGATCG 26

273 cércéradrirdiredédaridared 298

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Search completed: November 17, 2004, 02:10:51 Job time : 361.388 secs

us-09-821-782e-2.rnpb

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November 16, 2004, 23:47:45; Search time 38.7763 Seconds (without alignments) 3621.431 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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26
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Perfect score:
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Result No.	Score	Query	Query Match Length DB ID	DB	ID	Description
c1	24.4	93.8	!	9	US-09-960-352-9412	Sequence 9412, Ap
ر ن	24.4	93.8		6	US-09-960-352-3962	Sequence 3962, Ap
ص ع	24.4	93.8	241	σ	US-09-960-352-5417	Sequence 5417, Ap
Ω 4	24.4	93.8		σ	US-09-960-352-3998	Sequence 3998, Ap
c S	24.4	93.8		σ	US-09-960-352-12066	Sequence 12066, A
و ن	24.4	93.8		6	US-09-960-352-9213	Sequence 9213, Ap
7	24.4	93.8		σ	US-09-960-352-13007	Sequence 13007, A
ფ	24.4	93.8		σ	US-09-960-352-2332	Sequence 2332, Ap
ი ი	24.4	93.8		6	US-09-960-352-8757	Sequence 8757, Ap
c 10	24.4	93.8		σ	US-09-960-352-1158	Seguence 1158, Ap
c 11	24.4	93.8		σ	US-09-960-352-5211	Sequence 5211, Ap
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	17	22.8	87.7	231	14	US-10-146-502-824	
	18	22.8	87.7	308	14	US-10-066-543-2469	2469,
	19	22.8	87.7	314	14	US-10-066-543-2374	2374,
O	20	22.8	87.7	317	16	US-10-242-535A-11785	
υ	21	22.8	87.7	317	16	US-10-085-783A-11785	
υ	22	22.8	87.7	337	15	US-10-341-434-172	Sequence 172, App
Ö	23	22.8	87.7	341	16	US-10-242-535A-36990	
U	24	22.8	87.7	341	16	US-10-085-783A-36990	
	25	22.8	87.7	376	14	US-10-066-543-2414	
	56	22.8	87.7	376	14	US-10-066-543-2481	
υ	27	22.8	87.7	400	16	US-10-242-535A-10725	
υ	28	22.8	87.7	400	16	US-10-085-783A-10725	
	29	22.8	87.7	404	14	US-10-066-543-1961	
υ	30	22.8	87.7	421	10	US-09-918-995-5261	
	31	22.8	87.7	433	14	US-10-060-036-875	875, A
	32	22.8	87.7	469	14	US-10-060-036-1324	1324
	33	22.8	87.7	578	σ	US-09-879-536-763	763,
	34	22.8	87.7	591	10	US-09-871-161-493	Sequence 493, App
	35	22.8	87.7	597	σ	US-09-879-536-562	Sequence 562, App
	36	22.8	87.7	619	10	US-09-871-161-510	
	37	22.8	87.7	899	σ	US-09-879-536-812	
O	38	22.8	87.7	793	18	US-10-484-364-53	
O	39	22.8	87.7	1004	18	US-10-484-364-38	38,
U	40	22.8	87.7	1082	15	US-10-139-794-50	
υ	41	22.8	87.7	1107	10	US-09-822-846-298	298,
O	42	22.8	87.7	1140	15	US-10-325-881-7	
υ	43	22.8	87.7	1213	σ	US-09-925-301-325	Sequence 325, App
U	44	22.8	87.7	1214	15	US-10-106-698-2047	Sequence 2047, Ap
O	45	22.8	87.7	1955	15	US-10-170-385-208	Sequence 208, App
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RES	RESULT 1						
ns.	96-60-	US-09-960-352-9412/c	112/c				
•-	equen	Sequence 9412, Application US/09960352	Applic	ation	us/o	9960352	

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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 9412
LENGTH: 200
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 40-LIB34-065-Q1-E1-B12
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llarity 96.2%; Pred, No. 0.2;
Conservative 0; Mismatches 1;
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US-09-960-352-3962/c
Sequence 3962, Application US/09960352
; Patent No. US20020137139A1
Patent No. US20020137139A1
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Best Local Similarity
                         GENERAL INFORMATION:
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Best Local Similarity 96.2%;
Watches 25; Conservative (
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96.2%;
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Best Local Similarity 96.2
Matches 25, Conservative
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Best Local Similarity
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  SEO ID NO 3998
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           APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND CTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3962
LENGTH: 235
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nembing
APPLICANT: Tao, Nembing
APPLICANT: Tao, Nembing
APPLICANT: Batt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21 (10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5417
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APPLICANT: Tao, Wenghing
APPLICANT: Tao, Wenghing
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10299)C
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                                                                                                                                                                                                                                                                                                 ORGANISM: Bos taurus
COTHER INFORMATION: Clone ID: 17-LIB34-051-Q1-E1-E1
US-09-960-352-3962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 23-LIB34-052-Q1-E1-F3
US-09-960-352-5417
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Pred. No. 0.21;
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CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Patent No. US20020137139A1
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Patent No. US20020137139A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               93.8%;
96.2%;
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Best Local Similarity 96.2
Matches 25; Conservative
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Best Local Similarity 96.2
Matches 25; Conservative
GENERAL INFORMATION:
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US-09-960-352-3998/c
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Sequence 9213, Application US/09960352

Sequence 9213, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, NuGible AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 9213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-BOVMS1-008-Q1-E1-E8
US-09-960-352-12066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGANISM: Bos taurus

; OrGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 40-BOVMS1-002-Q1-E1-B8

US-09-960-352-9213
TYPE: DNA
CRGANISM: Bos taurus
CHER INFORMATION: Clone ID: 17-LIB34-084-Q1-E1-E9
US-09-960-352-3998
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US-09-960-352-12066/c
Squence 12066, Application US/09960352
Fatent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND CTHER MOLECUI
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SERVID NO 12066
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Pred. No. 0.23;
0; Mismatches 1;
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د.
                                                                                                                          DB .22;
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                                                                                                                                                                       0; Mismatches
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                                                                                                                          Score 24.4;
Pred. No. 0.
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# APPLICANT: Tao, Nengbing
# APPLICANT: Byatt, John C.
# APPLICANT: Mathialagan, Nagappan
# TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
# TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
# CURRENT APPLICATION NUMBER: US/09/960,352
# CURRENT FILING DATE: 2001-09-24
# NUMBER OF SEQ ID NOS: 15112
# SEQ ID NO 8757
# LANDAUM.
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERBNCE: 16511.006/37-21 [10298]C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1158
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MOSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
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OTHER INFORMATION: Clone ID: 06-BOVMS1-014-Q1-E1-B5
                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757
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Pred. No. 0.23;
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ilarity 96.2%; Pred. No. 0.23;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.8%;
Best Local Similarity 96.2%;
Matches 25; Conservative
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ORGANISM: Bos taurus
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Les 25; Conserv
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US-09-960-352-1158/c
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LOCATION: (422)
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Matches
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Batent No. US20020137139A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13007
LENGTH: 417
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: MUGCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFERMATION: Clone ID: 56-BOVMS1-006-Q1-E1-F12
US-09-960-352-13007
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US-09-960-352-2332
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                                                                                                                                                            115 ccrccracriciredecaricares 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2332, Application US/09960352 Patent No. US20020137139A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 25; Conserv
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US-09-960-352-2332/c
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US-10-085-783A-44171/c
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                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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Sequence 1164, Application US/09876143
Publication No. US20040081958A1
GENERAL INFORMATION:
APPLICANT: Infigen Inc.
APPLICANT: ELIERTENN, KENNETH J.
APPLICANT: CHILDS, LYNETTE
APPLICANT: CHILDS, LYNETTE
APPLICANT: FORSYTHE, TODD
APPLICANT: FORSYTHE, TODD
APPLICANT: FORSYTHE, TODD
TITLE OF INVENTION: CELLULAR REPROGRAMMING
FILE REFERENCE: 028040-0202
CURRENT APPLICATION NUMBER: US/09/876,143
CURRENT APPLICATION NUMBER: 06/203,874
PRIOR APPLICATION NUMBER: 60/203,874
PRIOR APPLICATION NUMBER: 60/203,874
SPRIOR APPLICATION NUMBER: 60/203,874
SPRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 1744
SSEQ ID NO 1164
LENGTH: 979
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis FILE REPERSURE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
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                                                                                                                                                                                                                                                                                 Score 24.4; DB 9; Length 475; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                      LOCATION: (7), (423)
OTHER INFORMATION: unsure at all n locations
CTHER INFORMATION: Clone ID: 23-BOVMS1-009-Q1-F11
US-09-960-352-5211
                                                                                                                                                                                                                                                                               Query Match
93.8%; Score 24.4; D
Best Local Similarity 96.2%; Pred. No. 0.23
Matches 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1). (979)
; OTHER INFORMATION: n is a, c, g, or t
US-09-876-143-1164
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CURRENT FILING DATE: 2001-0
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5211
LENGTH: 475
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Matches 25; Conservative
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                                                                                                        ORGANISM: Bos taurus
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US-10-242-535A-44171/c
                                                                                                                            FEATURE:
NAME/KEY: unsure
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US-09-876-143-1164/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bovine
                                                                                        TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 44.71
                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Patent No. US2002017552A1

GENERAL INFORMATION:

APPLICANT: Jiang, Yuqiu

APPLICANT: Jiang, Yuqiu

APPLICANT: Gecrist, Heather

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITION AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.527

CURRENT APPLICATION NUMBER: US/09/878,178

CURRENT PILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                           Length 120;
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Pred. No. 1;
0; Mismatches
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0; Mismatches
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR PILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PATENTIN VETSION 3.2
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Pred. No. 1;
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Best Local Similarity 92.33
Matches 24; Conservative
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Best Local Similarity 92.3
Matches 24; Conservative
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; SEQ ID NO 824
; LENTH: 231
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; MAME/KEY: misc_feature
; LOCATION: (1)...(231)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-824

Query Match

Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY | CCTCCTAGTTTGTTAGGGATTGATCG 26
Db 199 CCTCCTAGTTTGTTAGGGATCG 224
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Search completed: November 17, 2004, 03:11:51 Job time: 40.7763 secs

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LENGTH: 578
RESULT 2
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Sequence 562, App
Sequence 510, App
Sequence 7, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 375, App
Sequence 375, App
Sequence 375, App
Sequence 375, App
Sequence 3609, App
Sequence 1042, App
Sequence 107, Appli
                                                              November 16, 2004, 23:55:00 ; Search time 9.24665 Seconds (without alignments) 1998.616 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                        / cgn2_6/ptodata/l/ina/5A COMB.seq:*
2: /cgn2_6/ptodata/l/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/l/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/l/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/l/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/l/ina/PCTUS COMB.seq:*
        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-513-999C-22922
US-09-385-982-200
US-08-153-848-35
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US-09-313-294A-7516
US-09-596-002-37
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US-09-270-767-14799
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US-09-738-946-9
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US-09-525-906-1
US-09-989-2
US-09-377-856-1
US-09-377-856-1
US-09-302-681-2
US-09-303-611-1
US-10-053-611-1
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US-09-328-111-812
                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-328-111-562
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                                                                                                                                                                         824507 seqs, 355394441 residues
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                                                                                                                          1 cctcctagtttgttagggattgatcg
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Maximum Match 100%
Listing first 45 summaries
                                              nucleic search, using sw model
                                                                                                                                             IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                               seq length: 0
seq length: 200000000
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Match Length DB
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Sequence 35, Appl
Sequence 35, Appl
Sequence 12, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 5, Appli
Sequence 2479, Ap
Sequence 370, App
Sequence 370, App
Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 763, Application US/09328111

Eaquence 763, Application US/09328111

Eaquence 763, Application US/09328111

SERVERAL INFORMATION:

APPLICANT: Endege, Wilson O.

APPLICANT: Burgess, Christopher C.

APPLICANT: Burgess, Christopher C.

APPLICANT: Carroll III, Eddie

APPLICANT: Carroll III, Eddie

APPLICANT: Carroll III, Eddie

APPLICANT: Derti, Adman

APPLICANT: Derti, Adman

APPLICANT: Derti, Adman

APPLICANT: Lewis, Marcia E.

APPLICANT: Nonahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: NOVEL HUMAN

TITLE OF INVENTION: NOVEL HUMAN

TITLE OF INVENTION: NOVEL HUMAN

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-06-10

NUMBER OF SEQ ID NOS: 850

NUMBER OF SEQ ID NOS: 850

SOFTHARE: FREEEEE FREEEE FREEEE FREEEEE FREEEEE
  US-09-299-843A-35
US-09-088-337B-35
PCT-US91-11153-35
US-09-270-767-12161
US-08-452-075-1
US-09-231-061-1
US-09-011-762-5
US-09-107-532A-2479
US-09-107-532A-2479
US-09-107-532A-3287
US-09-107-532A-3287
US-08-307-382-3
US-08-307-382-3
US-08-478-727-3
US-08-478-727-3
US-08-478-727-3
US-08-478-727-3
US-08-478-727-3
US-08-478-727-3
US-08-478-75-3
US-08-934-254-3
US-08-934-254-3
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; Sequence 493, Application US/09385982
Patent No. 6262334
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , LOCATION: (1)...(578)
, OTHER INFORMATION: n = A,T,C or G
US-09-328-111-763
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Best Local Similarity 92.3
Matches 24; Conservative
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ORGANISM: Homo sapiens
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Pred. No. 0.054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | PATENT NO. 9.522333 |
| PATENT NO. 9.522333 |
| APPLICANT: Endege, Wilson O. |
| APPLICANT: Steinmann, Kathleen E. |
| APPLICANT: Astle, Jon H. |
| APPLICANT: Burgess, Christopher C. |
| APPLICANT: Bushnell, Steven E. |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Carroll III, Eddie |
| APPLICANT: Carroll Marcia E. |
| APPLICANT: Ford, Donna M. |
| APPLICANT: Ford, Donna M. |
| APPLICANT: Schlegel, Marcia E. |
| APPLICANT: Schlegel, Monahan, John E. |
| APPLICANT: Schlegel, Nobert E. |
| TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION |
| TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION |
| FILE REFERENCE: CCD-257 (US) |
| CURRENT APPLICATION NUMBER: US 60/088,801 |
| EARLIER FILING DATE: 1998-06-10 |
| SARLIER FILING DATE: 1998-06-10 |
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REPERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER PILING DATE: 1999-06-08
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1998-01-27
EARLIER PILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOUTWARE: FRSEESEQ for Windows Version 3.0
SEQ ID NO 493
LENGTH: 591
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-haa 2; Indels
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US-09-328-111-562
Sequence 562, Application US/09328111
; Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
JCCATION: (1)...(591)
US-09-385-982-493
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| LOCATION: (1)...(597)

| CTHER INFORMATION: n = A,T,C or G

US-09-328-111-562
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Best Local Similarity 92.3%;
Matches 24; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                 Sequence 510, Application US/09385982

| Sequence 510, Application US/09385982
| Patent No. 652334
| TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II
| PILE REFERENCE: CCDNA_260XX
| CURRENT APPLICATION NUMBER: US/09/385,982
| CURRENT FILING DATE: 1999-06-30
| EARLIER FILING DATE: 1999-06-30
| SALLIER RILING DATE: 1999-06-30
| SALLIER RILING DATE: 1999-06-31
| NUMBER OF SEQ ID NOS: 544
| SOFTWARE: FREESEQ FOR Windows Version 3.0
| LENGTH: 619
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Burges, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Marcia E.
APPLICANT: Monahan, John B.
APPLICANT: Monahan, John B.
APPLICANT: Monahan, John B.
APPLICANT: Monahan, John B.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION WINDER: US/09/328,111
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SECULORICAND SECULO
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205 cerecrastrierrassasacesares 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
i LOCATION: (1)...(619)
cother INFORMATION: n = A,T,C or G
US-09-385-982-510
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Conservative
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STATE: Washington
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                                       Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                   US-09-097-889-2/c
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US-09-525-906-1
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                                                                                                                                87.7%; Score 22.8; DB 3; Length 668; 92.3%; Pred. No. 0.055; ive 0; Mismatches 2; Indels
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CURRENT PILION DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 09/377,856
PRIOR APPLICATION NUMBER: 09/377,856
PRIOR APPLICATION NUMBER: 09/377,856
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR PILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 16568
                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09377497

Patent No. 6670119

GENERAL INFORMATION:
APPLICANT: YOSHIKAWA, YOSHIE
APPLICANT: MOTAI, HIROYUKI
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
APPLICANT: ATO, FUMITSUGU
APPLICANT: ATO, FUMITSUGU
APPLICANT: ATO, INUNOSHIN
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
FILE REFERENCE: 1422-388P
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1140
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CHER INFORMATION: any n or Xaa = unknown

US-09-377-497-7
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  ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(668)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-812
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Patent No. 6605433
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Sidransky, David
                                                                                                                                                                                24; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                              Best Local Similarity
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US-09-377-497-7/c
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APPLICANT: Herristadt, Corrina
APPLICANT: Ghosh, Soumitra S.

APPLICANT: Davis, Robert E.

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
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Length 16568;
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US-09-377-856-1/C
US-09-377-856-1/C
Sequence 1, Application US/09377856
Patent No. 6344322
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTER: DEM PC compatible
COMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: US-JUN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
DB 4;
Score 22.8; DI
Pred. No. 0.1;
0; Mismatches
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NAME: ROSEDMEND D., Stephen J.
REGISTRATION NUMBER: 43,058
REGISTRATION NUMBER: 660088.417
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. 6218117
92.3%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                     ATTORNEY/AGENT INPORMATION:
NAME: ROSenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 66008.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/10053611; Patent No. 6750021
                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
TYPE: nucleic acid
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Best Local Similarity 92.3%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
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ORGANISM: Homo sapiens
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US-09-098-079-2
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Patent No. 6499095;
GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Glocab, Soumitra S.
APPLICANT: Glevenger, William
APPLICANT: Glevenger, William
APPLICANT: Glevenger, William
APPLICANT: Davis, Robert B.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Herristadt, Corrina
APPLICANT: Glosh, Soumitra S.
APPLICANT: Glosh, Soumitra S.
APPLICANT: Glosh, Soin F.
TOTAL CANT: Paby, Eoin F.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: QUANTIFICATION OF EXTRAMITOCHONDRIAL DNA
FILE REFERENCE: 66008-41661
CURRENT APPLICATION NUMBER: US/09/302,681
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                    Score 22.8; DB 3;
Pred. No. 0.1;
0; Mismatches 2;
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               CURRENT APPLICATION NUMBER: US/09/377,856
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 16569
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US-09-302-681-2/c
; Sequence 2, Application US/09302681
; Patent No. 6441149
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.3%;
Matches 24; Conservative
1107.82346
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; ORGANISM: Homo sapiens
US-09-377-856-1
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; ORGANISM: Homo sapien
US-09-302-681-2
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Best Local Similarity
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FILE REFERENCE:
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US-09-098-079-2/c
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STATE: Ware COUNTRY:
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     DB 4; Length 16569;
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Markers
FILE REPERENCE: 1107,82346
CURRENT APPLICANTON NUMBER: US/10/053,611
CURRENT FILING DATE: 2002-01-24
                                                    Indels
Score 22.8; D
Pred. No. 0.1;
0; Mismatches
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PRIOR FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                                                                                   1 CCTCCTAGITIGITAGGGATIGATCG
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US-08-647-584-46/c
; Sequence 46, Application US/08647584
; Patent No. 5786144
; GENERAL INFORMATION:
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81.5%;
                                                                                                                     Local Similarity 88.5
hes 23; Conservative
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ORGANISM: Zea mays
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US-09-385-982-375
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SEQ ID NO 7516
                                                                                     Query Match
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                                                                                                                                                                       Matches
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APPLICANT: De Salle, Rob
APPLICANT: Birstein, Vadim J.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR
TITLE OF INVENTION: IDENTIFICATION OF SPECIES ORIGIN OF CAVIAR
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weil, Gotshal & Manges LLP
STREET: 2882 Sand Hill Road, Suite 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
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GENERAL INFORMATION:

APPLICANT: ENDEGGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX;

CURRENT PILING DATE: 1999-08-30

EARLIER PILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-01-27

SAPINGRENCE SEQ ID NOS: 544

SOUTHARE: FESESEQ for Windows Version 3.0

LENTH: 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/647,584
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Baran, Alexandra J.
REGISTRATION NUMBER: 39,101
REFERENCE/DOCKET NUMBER: 14503.4010
TELECOMMINICATION INFORMATION:
TELECHONE: (415) 926-6200
TELEPHONE: (415) 926-6200
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCTCCTAGTTTGTTAGGGATTGATCG 26
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                                                                                                                                                                                                                                                                                                     STREET: 2882 Sand Hill Road, Suite CITY: Menlo Park STATE: California COUNTRY: U.S.A. ZIP: 94025 COMPITER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 375, Application US/09385982
Patent No. 6262334
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Homo sapiens
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Sequence 7516, Application US/09313294A

Patent No. 6476212

Patent No. 6476212

Patent No. 6476212

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Sherman, Baradley K.

TITLE OF INVENTION: POLYNUGLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

FILLE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600
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80.0%; Score 20.8; DB 4; Length 315;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 22; Conservative 0; Mismatches 4; Indels
     Length 602;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMES/KEX: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700381866H1
NAMES/KEY: UNBURE
LOCATION: 32, 56, 84, 87, 117-118, 160, 196, 244
OTHER INFORMATION: a, t, c, g, or other
Score 21.2; DB 3; Pred. No. 0.33; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 17, 2004, 03:15:11 Job time : 11.2467 secs
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                                                                                                               1 CCTCCTAGTTTGTTAGGGATTGATCG 26
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Abg83297 Cytochrom
Abx49123 Bovine ES
Abx41392 Bovine ES
Abx41392 Bovine ES
Abx42082 Bovine ES
Abx42631 Bovine ES
Abx44209 Bovine ES
Abx44209 Bovine ES
Abx44209 Bovine ES
Abx439507 Bovine ES
Abx439507 Bovine ES
Abx430950 Bovine ES
Abx46099 Bovine ES
Abx461849 Bovine ES
Abx46538 Bovine ES
Abx45538 Bovine ES
                                                          November 16, 2004, 16:25:24 ; Search time 40.7744 Seconds (without alignments) 3218.578 Million cell updates/sec
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Abx47053
Abx42249
Abx432249
Abx33507
Abx335955
Abx37092
Abx46099
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Abx4538
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Abx37811
Abx37811
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          Compugen Ltd.
GenCore version 5.1.6 (c) 1993 - 2004 Compu
                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                            4134886 segs, 2624710521 residues
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Maximum Match 100%
Listing first 45 summaries
                                          sw model
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ABX41849
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ABX44580
ABX35249
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ABX49123
ABX41392
ABX41185
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ABX44209
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ABX39507
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ABX35955
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Gapop 10.0 , Gapext 1.0
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geneseqn2003ds:*
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Maximum DB seq length: 200000000
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Perfect score:
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322	32	œ	472	ö	25
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792 Bovine	ABX38792	ω	455	ċ	25
5 Bovine	ABX37805	œ	448	00	25
Bovine	ABX38849	œ	447	99	52
Bovine	ABX39586	α	447	100.0	25
Bovine E	309	æ	446	00	25
Bovine	ABX47632	Φ	446	100.0	25
Bovine	ABX44982	æ	445	0	25
Bovine	ABX40780	œ	444	00	52
Bovine	ABX43069	œ	443	00	25
Abx36609 Bovine ES	ABX36609	œ	436	00	25
Abx44491 Bovine ES	ABX44491	œ	435	ö	25
Bovine E	ABX47629	æ	433	00	25
Abx42116 Bovine ES	ABX42116	œ	432	100.0	25
Abx46840 Bovine E	ABX46840	œ	429	00	25
Bovine E	ABX40056	œ	428		25
Bovine E	ABX44677	α	425	ö	25
Bovine E	ABX39981	σ	424	00	25
6 Bovine	ABX47816	œ	422	ö	25
9415 Bovine E	ABX39415	œ	421	٥.	25

ALIGNMENTS

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Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; PCR primer; ss.
                                                                                                                                                                                                                                 Cytochrome b gene universal PCR primer mcb 398 SEQ ID NO:2.
                                                            BP.
                                                            ABQ83297 standard; DNA; 25
                                                                                                                                                                        18-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                          Mitochondrial
                                                                                                                  ABQ83297;
RESULT 1
ABQ83297
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WO200277278-A1 03-OCT-2002 Synthetic

(COUL) COUNCIL SCI & IND RES. 28-MAR-2001; 2001WO-IN000055 28-MAR-2001; 2001WO-IN000055 Verma SK, Singh L;

WPI; 2003-018945/01.

New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.

Claim 1; Page 116; 128pp; English.

The present invention describes universal primers, mcb 398 and mcb 869 (see ABQ81297 and ABQ83298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of

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biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal bunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal crimingue for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime origin of blood found at the scene of the crime in animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                converted to a commercial molecular kit a for wildlife identification in forensics
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Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

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Gaps
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0
Query Match
100.0%; Score 25; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 25; Conservative 0; Mismatches 0; Indels
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0

1 TACCATGAGGACAAATATCATTCTG 25 TACCATGAGGACAAATATCATTCTG 25

8

ABX49123 standard; cDNA; 329 BP. ABX49123; RESULT 2 ABX49123

Bovine EST associated with lactation/muscle/fat deposition #14288. (first entry) 21-FEB-2003

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

Bos Taurus

US2002137139-A1.

26-SEP-2002.

24-SEP-2001; 2001US-00960352.

12-JAN-1999; 99US-0115707P 11-JAN-2000; 2000US-00480902

(BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. (TAON/) TAO N. (WARR/) WARREN W C.

Warren WC; Tao N, Mathialagan N, Byatt JC,

WPI; 2003-110599/10.

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Claim 2; SEQ ID NO 14288; 245pp; English.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences,

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

WPI; 2003-110599/10.

Claim 2; SEQ ID NO 6557; 245pp; English

cc appearing as ABX34836-ABX49947, or complements of them. Also included are cci acid linked to a promoter and a 3' non- translated sequence that cfunctions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cc polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cci (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or crissue, where hybridisation between the marker nucleic acid and the ccomplementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the detecting the level or pattern of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. Cc level or pattern of complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. Cc for genetically improving cattle. The present sequence is one of the cci for genetically improving cattle. The present sequence is one of the cc sequence was not shown in the specification but was obtained in celectronic format from the USPTO web site:

Cc seqdata.uspto.gov/sequence.html?DocID=20020137139 ô Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Gaps Bovine EST associated with lactation/muscle/fat deposition #6557 .; 0 100.0%; Score 25; DB 8; Length 329; 100.0%; Pred. No. 0.26; 0; Indels Sequence 329 BP; 96 A; 78 C; 66 G; 89 T; 0 U; 0 Other; Warren WC; Mismatches 305 TACCATGAGGACAAATATCATTCTG 329 1 TACCATGAGGACAAATATCATTCTG 25 Tao N, / Match Local Similarity 100.0%; Pr ABX41392 standard; cDNA; 346 BP 24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902. 20-FEB-2003 (first entry) Byatt JC, Mathialagan N, (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. (WARR/) WARREN W C. US2002137139-A1. 26-SEP-2002. Bos Taurus. ABX41392; Query Match (TAON/) Matches RESULT 3 à 셤 NAME OF A STATE OF A S

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cattle, and the LMRD nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMRD), derived from cattle, and the LMRD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences.

Concleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX4937, or complements of them. Also included are if il a transformed cell having a nucleic acid comprising an LMRD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and control of polyadenylated ribonucleotides to a 3' end of the maching any configurating; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complementary nucleic acid sequences or its complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is used for the detection of the molecule; TME LMPD nucleic acid is used for level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                       It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in
                       invention relates to a purified nucleic acid molecule associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine, 88; BST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Score 25; DB 8; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segdata.uspto.gov/seguence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 TACCATGAGGACAAATATCATTCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TACCATGAGGACAAATATCATTCTG 25
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11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABX41185 standard; cDNA; 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Syatt JC, Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-110599/10.
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from a cattle. And the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences.

Complements as ABX34836-ABX49947, or complements of them. Also included are contained to a promoter and a 3 non-translated sequence that the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cc of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cc itssue comprising a level or pattern of a molecule in a bovine cell or tissue complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, the detection of the complementary nucleic acid predictive of the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for complementary nucleic mattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle conformation preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the complement sequence was not shown in the present sequence was not shown in the present sequence is not shown in the present or pattern of shorters and analysis, and incomplement sequence was not shown in the present sequence is one the incomplement of shorters are not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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Pred. No. 0.27;
); Mismatches 0; Indels
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                                                                                      Claim 2; SEQ ID NO 6350; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            format from the USPTO web si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 TACCATGAGGACAAATATCATTCTG 348
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11-JAN-2000; 2000US-00480902.
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MATHIALAGAN N.
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Best Local Similarity
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WARREN W C.
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The invention relates to a purilled nucleic acid molecule absolutated with actuation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second molecule comprising any of 15112 nuclectide sequences.

The invention as ABX34836-ABX49947, or complements of them. Also included are appearing as ABX34836-ABX49947, or complements of them. Also included are in a transformed cell having a nucleic acid comprising an LMFD nucleic caid linked to a promoter and a 3, non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue. The detection of the complementary nucleic acid is predictive of the complementary nucleic acid molecule. The LMFD nucleic acid is used for level or pattern of the molecule. The LMFD molecule caid is used for the complementary nucleic acid is used for the detection of the molecule. The LMFD molecule acid an analysis, cattle complementary profits and not an marker of the molecule in a bovine cell or tissue. The present sequence is one of the complementary profit and analysis, cattle complementary profit and profit acid some of the complementary profit and analysis, cattle complementary profit and molecule in a portine cell or the complementary profit and paint and the present sequence was not shown in the specification but was obtained in a part of part or pattern of a pattern of a pattern of a molecule and pattern of a molecule acid is present sequence and the marker page of the complementary profit and pattern of a molecule acid is predictive of the complementary 
                                                                                                                                                                                                                                                                                                                              The invention relates to a purified nucleic acid molecule associated with
                                                                                                                                       New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 25; DB 8; Length 380; Pred. No. 0.27;
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100.0%; Pred. No.
                         Warren WC;
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                                                                                                                                                                                                                                                                        Claim 2; SEQ ID NO 7247; 245pp; English
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                            Tao N,
                            Mathialagan N,
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Best Local Similarity 100.0
Matches 25; Conservative
                                                                                     WPI; 2003-110599/10.
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                            Byatt JC,
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0; Indels 174 TACCATGAGGACAAATATCATTCTG 198 g

ABX36231 standard; cDNA; 388 BP 20-FEB-2003 (first entry) ABX36231; THE STANDARD STANDARD

Bovine EST associated with lactation/muscle/fat deposition #1396.

Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding

Bos Taurus

US2002137139-A1.

26-SEP-2002

24-SEP-2001; 2001US-00960352.

12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902.

BYATT J C. MATHIALAGAN N. TAO N. (BYAT/) (MATH/) TAON/)

(WARR/) WARREN W C.

Warren WC; Tao N, Byatt JC, Mathialagan N,

WPI; 2003-110599/10.

and muscle and fat identification and analysis, deposition, useful for genome mapping, gene identific cattle breeding, or for genetically improving cattle New nucleic acid associated with lactation,

Claim 2; SEQ ID NO 1396; 245pp; English.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are complements acid linked to a promoter and a 3 non-translated sequence that continued in the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and complementary nucleic acid sequences or its complement or fragment in a bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the molecule of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle correction of the MFD EST (expressed sequence et al) nucleic acids. Note: The present sequence was not shown in the sequence cide in the context of the nucleus of the context of the molecule of the nucleus of the nucleus of the nucleus of the nucleus one of the context sequence was not shown in the sequence cides one of the nucleus of seqdata.uspto.gov/sequence.html?DocID=20020137139 format from the USPTO web site: electronic

Sequence 388 BP; 118 A; 111 C; 56 G; 101 T; 0 U; 2 Other;

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Gaps

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Gaps ; 0 100.0%; Score 25; DB 8; Length 388; 100.0%; Pred. No. 0.27; 0; Indels 0; Mismatches Local Similarity 100. es 25; Conservative Query Match Matches

0

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RESULT 7

ABX42640 standard; cDNA; 397 ABX42640; ABX42640

20-FEB-2003 (first entry)

Bovine EST associated with lactation/muscle/fat deposition #7805

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

Bos Taurus.

US2002137139-A1

26-SEP-2002

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24-SEP-2001; 2001US-00960352.
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                                                                                                                                                                                                                                                                                     (WARR/) WARREN W C.
                                    US2002137139-A1.
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Bos Taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ruciels acid molecule comprising any of 19112 incleolide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid molecule obtained from the bovine cell or cissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or itssue, where hybridisation between the marker nucleic acid, where the detection of the complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the 1512 bovine LMFD BST (expressed sequence tag) nucleic acids. Note: The present sequence is some of in the money.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleitide sequences,
                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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                                                                                                                                                                                                                                 Warren WC;
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                     24-SEP-2001; 2001US-00960352
                                                            12-JAN-1999; 99US-0115707P
11-JAN-2000; 2000US-00480902
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Best Local Similarity 100.09
Matches 25; Conservative
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                                                                                                                                                                                                                               Byatt JC, Mathialagan N,
                                                                                                                         (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                        WPI; 2003-110599/10.
                                                                                                                                              (MATH/) MATHIALAGAN
(TAON/) TAO N.
(WARR/) WARREN W C.
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The invention relates to a purified nucleic acid molecule associated with catation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising an upper discally hybridise to a second are appearing as ABX34836-ABX49947, or complements of them. Also included are (i) in a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3 non- translated sequence that a cinctions in the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3 end of the mRNA molecule, and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule, and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the detection of the molecule. The LMFD nucleic acid is used for the molecule or pattern of a molecule in a bovine cell or tissue. Complementary nucleic acid is predictive of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. Complementary nucleic acid is predictive of the complementary nucleic acid is bovine and snalysis, cattle for genetically improving cattle. The present sequence is one of the complement sequence was not shown in the specification but was obtained in pattern of present sequence is not shown in the specification but we apterned in
                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 402 BP; 125 A; 107 C; 62 G; 108 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                           Tao N, Warren WC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 12218; 245pp; English.
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Best Local Similarity 100.0
Matches 25; Conservative
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BYAT/) BYATT J C. MATH/) MATH/ALAGAN N.
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RESULT 8 ABX47053

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(first entry)

20-FEB-2003

ABX42249;

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMPD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences.

(1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that acid linked to a promoter and a 3' non-translated sequence that clunctions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the nucleic acid permits the detection of the complementary nucleic acid permits the detection of the level or pattern of the complementary nucleic acid permits for use complementary nucleic acid permits for use complementary nucleic acid permits for the detection of the molecule. The LMFD nucleic acid is used for the evel or pattern of the molecule in a bovine cell or tissue.

C determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle C breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the reader and mannalysis and incleic admits in the incleic admits in the molecule in a point in the incleic admits in the molecule in a molecule in a point in the incleic admits in the molecule in a point in the incleic admits in the molecule in a point in the incleic admits in the molecule in a point in the incleic admits in the molecule in a molecule in a mo
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                        Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
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shown in the specification but was obtained in
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11-JAN-2000; 2000US-00480902
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                                                                                                                                                                                                                                                                                                                                                                                                                    (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
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                                                                                                                           Bos Taurus
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Gaps
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                            100.0%; Score 25; DB 8; Length 409; 100.0%; Pred. No. 0.27;
Sequence 409 BP; 127 A; 108 C; 62 G; 112 T; 0 U; 0 Other;
                                        0.27;
hes 0; Indels
                                                         Mismatches
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Best Local Similarity 100.0.
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379 TACCATGAGGACAAATATCATTCTG 403
 25
TACCATGAGGACAAATATCATTCTG
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373 TACCATGAGGACAAATATCATTCTG 397

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ABX42249 standard; cDNA; 409 BP.
RESULT 10
               ABX42249
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences.

C mucleic acid molecule comprising any of 15112 nucleotide sequences.

C that renafizationed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that c functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and compensations a lincubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid sequences or its complementary nucleic acid permits the detection of the molecule; and complementary nucleic acid sequence is nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the complementary nucleic acid is predictive of the the detection of the molecule. The LMFD nucleic acid is used for the complementary nucleic acid is predictive of the complementary nucleic acid is predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis,
                                                                                                                                       Bovine, ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
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cattle breeding, or for genetically improving cattle.
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nuclectide sequences, appearing as ABX34836-ABX493497, or complements of them. Also included are cid il a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule acid is predictive of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the suseful for genome mapping, gene identification and analysis, cattle breach sequence was not shown in the specification but was obtained in present sequence was not shown in the specification but was obtained in the present sequence and in the specification but was obtained in the present sequence was not shown in the specification but was obtained in the present sequence and the best of the sequence was not shown in the specification but was obtained in a boven the lattern and the lattern an
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                                                                                                                                                                                                                                             Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                   Bovine EST associated with lactation/muscle/fat deposition #4672.
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                                                  ABX39507 standard; cDNA; 409 BP.
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11-JAN-2000; 2000US-00480902.
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(TAON/) TAO N.
(WARR/) WARREN W C.
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                                                                                                    ABX39507;
RESULT 11
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New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                             Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                             Bovine EST associated with lactation/muscle/fat deposition #8498.
                                                                                                                                                                                                                                                                                                        Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 8498; 245pp; English
         340 TACCATGAGGACAAATATCATTCTG 364
 25
1 TACCATGAGGACAAATATCATTCTG
                                                            ABX43333 standard; cDNA; 411 BP.
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carrie, and unitarious actual appointments of them. Also included are appearing as ABX34836-ABX49947, or complements of them. Also included are and in a transformed cell having a nucleic acid comprising an LMFD nucleic of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule; and complementary nucleic acid is predictive of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for complementary nucleic acid is predictive of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for the acet or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or complement from the USPID web site:

15112 bovine LMFD EST (expressed sequence as) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in collection and analysis. The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second seqdata.uspto.gov/sequence.html?DocID=20020137139

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Gaps

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Query Match

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Best Loca Matches

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gene analysis; cattle breeding.
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11-JAN-2000; 2000US-00480902.
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(MATH/) MATHIALAGAN N.
(TAON/) TAO N.
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                                                                                                                                                                                                                                                                                                                                                                                       ABX37092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementary incleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid, where level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and malysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                              Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                   Bovine EST associated with lactation/muscle/fat deposition #1120
                                                                            ;
0
                                    100.0%; Score 25; DB 8; Length 411; 100.0%; Pred. No. 0.27;
Sequence 411 BP; 130 A; 109 C; 61 G; 111 T; 0 U; 0 Other;
                                                                          Indels
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                                              100.0%; Prec. ....
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                                                                                                                                         378 TACCATGAGGACAAATATCATTCTG 402
                                                                                                                 1 TACCATGAGGACAAATATCATTCTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tao N,
                                                                                                                                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JAN-1999; 99US-0115707P,
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                    ABX35955 standard; cDNA; 412
                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARREN W C.
                                                    Local Similarity
nes 25; Conserv
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TAO N.

(MATH/) (TAON/) WARR/)

26-SEP-2002.

Bos Taurus

20-FEB-2003

ABX35955;

ABX35955

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated IMPD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nuclectide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are contained to a promoter and a 3 non-translated sequence that acid linked to a promoter and a 3 non-translated sequence that control or polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and of polyadenylated ribonuclectides to a 3' end of the mRNA molecule; and comprising a level or pattern of a molecule in a bowine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bowine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bowine cell or tissue, there is nucleic acid molecule obtained from the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid, where the detection of the complementary nucleic acid, where
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15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 8; Length 412; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Sequence 412 BP; 118 A; 108 C; 61 G; 125 T; 0 U; 0 Other;
                                                                                                                                                        segdata.uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 TACCATGAGGACAAATATCATTCTG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TACCATGAGGACAAATATCATTCTG 25
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level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine EST associated with lactation/muscle/fat deposition #11264.
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                                                                                                                                                                                                                                Score 25; DB 8; Length 413; Pred. No. 0.27;
                                                                                                                                                                                              Sequence 413 BP; 130 A; 109 C; 62 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                electronic format from the USPTO web site:
segdata.uspto.gov/sequence.html?DocID=20020137139
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                                                                                                                                                                                                                                                                                                                                   384 TACCATGAGGACAAATATCATTCTG 408
                                                                                                                                                                                                                                                                                                             1 TACCATGAGGACAAATATCATTCTG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX46099 standard; cDNA; 414 BP
                                                                                                                                                                                                                                  100.08;
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11-JAN-2000; 2000US-00480902.
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                                                                                                                                                                                                                                                                     25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WARR/) WARREN W C.
                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BYAT/) BYATT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAO N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2003
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complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where level or pattern of the complementary nucleic acid, where level or pattern of a molecule; a predictive of the level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format, from the USPTO web site:
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Gary
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: Liqun
TITLE OF INVENTION: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: US/09/102.705
CURRENT PILLIO DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 719
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
RESULT 2
US-09-702-705-719
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                                                                                                                 November 16, 2004, 23:55:00; Search time 8.89101 Seconds (without alignments) 1998.616 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-702-705-719
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US-09-658-824-719
US-09-377-497-7
US-09-37-889-2
US-09-37-889-2
US-09-372-681-2
US-09-098-079-2
US-01-053-611-1
US-07-825-959-8
US-07-825-959-8
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US-09-383-316-95
US-09-788-847-48
US-09-790-417-255
US-08-647-584-9
US-08-647-584-11
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US-09-614-124B-719
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US-08-910-733-17
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Listing first 45 summaries
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                                                                                   nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 4131, Ap
Sequence 4131, Ap
Sequence 27053, A
Sequence 166, A
Sequence 166, A
Sequence 27053, Appl
Sequence 26, Appl
Sequence 273, Appl
Sequence 273, Appl
Sequence 2773, Appl
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Sequence 11513, Application US/09270767

Sequence 11513, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

NULleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11513
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US-07-971-160-35
US-08-336-241-35
US-08-41-35
US-08-4119-024-35
US-09-119-024-35
US-08-417-226-35
US-08-417-226-35
US-09-136-131-35
US-09-313-294A-4131
US-09-313-294A-4131
US-09-313-294A-4131
US-09-313-294A-4133
US-09-270-767-27053
US-09-270-767-27053
US-09-28-28-16
US-09-453-702B-166
US-09-459-039A-2273
US-09-489-039A-2273
US-09-489-039A-2273
US-09-489-039A-2273
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APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT PERLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                Query Match 80.8%; Score 20.2; DB 4; Length 255; Best Local Similarity 88.0%; Pred. No. 2.4; Matches 22; Conservative 0; Mismatches 3; Indels
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                    CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SEQ ID NO 719
LENGTH: 255
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Patent No. 6667154
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                                                                                                                                                                                                                                     ; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-1248-719
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NAME/KEY: misc_feature
LOCATION: (1)...(255)
OTHER INFORMATION: n = A,T,C or G
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Bangur, Chaitanya S.
Lodes, Michael A.
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.,
APPLICANT: Lodes, Michael A.,
APPLICANT: Fanger, Gary
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                            ORGANISM: Homo sapien
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                          TYPE: DNA
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 255
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Pred. No. 2.4;
0; Mismatches 3; Indels
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80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                          96 TCCCGTGAGGCCAAATATCATTCTG 120
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US-09-614-124B-719
is Sequence 719, Application US/09614124B
is Patent No. 6630574
is GENERAL INFORMATION:
is APPLICANT: Wang, Tongtong
is APPLICANT: Bangur, Chaitanya S.
is applicant: Lodes, Michael A.
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Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
                                      FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(255)

CTHER INFORMATION: n = A,T,C or G
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// LOCATION: (1)...(225)
// OTHER INFORMATION: n = A,T,C or
US-09-736-457-719
                                                                                                                                                                        Query Match
Best Local Similarity 88.0%;
Matches 22; Conservative
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Carter, Darrick
Retter, Marc
TYPE: DNA ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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US-09-736-457-719
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.8%; Score 20.2; DB 4; Length 1140; Best Local Similarity 88.0%; Pred. No. 3.1; Matches 22; Conservative 0; Mismatches 3; Indels 0
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APPLICANT: Sidransky, David
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: Fliss, Makiko
APPLICANT: Fliss, Makiko
TITLE OF INVENTION: Mitochondrial Dosimeter
FILE REFERENCE: 1107.85815
CURRENT APPLICATION NUMBER: US/09/525,906
CURRENT APPLICATION NUMBER: US/377,856
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
                                    APPLICANT: YOSHIKAWA, YOSHIE
APPLICANT: MARAI, HIROYUKI
APPLICANT: ARADA, KIYOZO
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
TITLE REFERENCE: 1422-389B
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 70
SOCIEMARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 1140
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Patent No. 6605433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.8
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; CORGANISM: Homo sapiens US-09-525-906-1
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LENGTH: 16568
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                                                         APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-478C8
CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 719
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.8%; Score 20.2; DB 4; Length 255; Best Local Similarity 88.0%; Pred. No. 2.4; Matches 22; Conservative 0; Mismatches 3; Indels
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APPLICANT: Fan, Lique
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE RERERENCE: 210.21.478C11
CURRENT APPLICATION NUMBER: US/09/658,824
CURRENT FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
i LOCATION: (1)...(255)
COTHER INFORMATION: n = A,T,C or G
US-09-589-184-719
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US-09-658-824-719
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US-09-377-497-7
; Sequence 7, Application US/09377497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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ORGANISM: Homo sapien
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SOFTWARE: FASTSEQ for
SEQ ID NO 719
LENGTH: 255
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                                                                                                                                                                                                                                                                                        TYPE: DNA
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Patent No. 6489095

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Clevenger, William
APPLICANT: Fahy, Boin F.
APPLICANT: Pahy, Boin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
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                                                                                    RESULT 12
US-09-302-681-2
Sequence 2. Application US/09302681
Sequence 2. Application US/09302681
Sequence 3. Application US/09302681
Setent No. 6441149
SETENT NO. 6441149
SEPLICANT: HORMATION:
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION OUNHER: US/09/302,681
CURRENT APPLICATION NUMBER: US/09/302,681
SOFTWARE OF SEC ID NOS: 108
SOFTWARE PESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 16569;
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ZIP: 98104

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-UUN-1998

TYASSTPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.8%; Score 20.2; DB 4;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3;
15144 TCCCGTGAGGCCAAATATCATTCTG 15168
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ATTORNEY/AGENT INFORMATION:
NAME: ROSENMEN Dh.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 2:
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ADDRESSEE: SEED and I
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 16569
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APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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US-09-377-856-1
Sequence 1, Application US/09377856
Sequence 1, Application US/09377856
Sequence 1, Application US/09377856
Sequence 1, APPLICANT:
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler Kenneth
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Markers
FILE REFERENCE: 1107-82346
CURRENT APPLICATION NUMBER: US/09/377,856
CURRENT FILING DATE: 1999-08-20
CURRENT FILING DATE: 1999-08-08
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR FILING DATE: 1998-08-00
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 3.0
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88.0%; Pred. No. 5.2;
.ive 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-UN-1998
CLIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
                                                                          STATE: Washington
COUNTRY: USA
STATE: Washington
COUNTRY: USA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 622-631
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 22; Conservative
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Best Local Similarity 88.0
Matches 22, Conservative
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US-09-377-856-1
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TOPOLOGY:
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APPLICANT: Clinio, George C.
APPLICANT: Lin, Lilly
TITLE OF INVENTION: METHOD FOR MEASURING THE INACTIVATION OF TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
CITY: San Francisco
STREET: California
COUNTRY: USA
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Pred. No. 5.2;
0; Mismatches 3; Indels 0:
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                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: POLYAK, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Markers
FILE REFERENCE: 1107, 82346
CURRENT APPLICATION NUMBER: US/10/053,611
CURRENT APPLICATION NUMBER: US/09/377,856
PRIOR FILING DATE: 1999-08-20
PRIOR PILING DATE: 1999-08-20
PRIOR PILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PASSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 16569
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Patent No. 6750021
                                                                                                                                       Query Match 80.8%;
Best Local Similarity 88.0%;
Matches 22; Conservative
             LENGTH: 16569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.0<sup>3</sup>
Matches 22; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                          ; TOPOLOGY: linear
US-09-098-079-2
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US-07-825-959-8/c
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US-10-053-611-1
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                                                                                                            November 16, 2004, 16:25:24; Search time 42.4054 Seconds (without alignments) 3218.578 Million cell updates/sec
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Abq83306 P
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Abx44247 R
Abx38797 R
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Abx47842
Abx37167
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Abx43592
Abx35993
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                4134886 segs, 2624710521 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM nucleic - nucleic search, using sw model
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ABX44048
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ABQ83332
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geneseqn1990s:*
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Maximum DB seq length: 200000000
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26
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                    Total number
                                                                                                                                                                                                                                   Sequence:
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C 22 24.4 93.8 472 8 ABQ83328 C 24 24.4 93.8 472 8 ABQ83303 C 25 24.4 93.8 472 8 ABQ83304 C 25 24.4 93.8 472 8 ABQ83304 C 27 24.4 93.8 472 8 ABX40046 C 29 22.8 87.7 210 10 ACD92164 31 22.8 87.7 210 10 ACD92164 C 33 22.8 87.7 230 10 ACD92164 C 35 22.8 87.7 310 10 ACD92164 C 35 22.8 87.7 340 5 ABV0825 C 36 22.8 87.7 340 4 AAI87354 C 36 22.8 87.7 414 4 AAI87354 C 36 22.8 87.7 419 4 AAI8933 C 41 22.8 87.7 419 4 AAI8933 C 41 22.8 87.7 419 4 AAI8933 C 42 22.8 87.7 419 4 AAI8933 C 43 22.8 87.7 419 4 AAI8933 C 44 22.8 87.7 421 4 AAI8049 C 44 22.8 87.7 434 4 AAI81714	Abq83328 Mitochond	Abg83303 Mitochond	Abg83304 Mitochond	Abq83326 Mitochond	Abq83337 Mitochond	Abx40046 Bovine ES	Abn74229 Bovine em	Aaa43716 Human sec	Acd93024 Human col	Abl37235 Human col	Acd92164 Human col	Abv08925 Human pro	Abv12642 Human pro	Acd92416 Human col	Aai82841 Human pol	Aai87354 Human pol	Aai87787 Human pol	Acd93031 Human col	Aai88933 Human pol	Ach18049 Human adu	Aai87673 Human pol	Abv95467 Human pan	Aai81714 Human pol	Abv95916 Human pan
22 24.4 93.8 472 25.2 24.4 93.8 472 26.2 24.4 93.8 472 28.2 24.4 93.8 472 29.8 29.8 22.8 87.7 23.0 33.2 22.8 87.7 33.0 34.2 22.8 87.7 33.0 35.2 22.8 87.7 33.0 35.2 22.8 87.7 33.0 35.2 22.8 87.7 33.0 35.2 22.8 87.7 33.0 35.0 22.8 87.7 33.0 35.0 22.8 87.7 33.1 41.4 22.8 87.7 42.1 42.2 887.7 42.1 42.2 887.7 42.1 42.2 887.7 43.4 42.5 887.7 443.5 22.8 87.7 7 443.5 22.8 87.7 7 443.5 22.8	ABQ83328	ABQ83303	ABQ83304	ABQ83326	ABQ83337	ABX40046	ABN74229	AAA43716		ABL37235		ABV08925	ABV12642		AA182841	AAI87354	AAI87787		AA188933	ACH18049	AA187673	ABV95467	AA181714	ABV95916
22 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 24.4 93.8 22.8 87.7 22.8 87.7 22.8 87.7 22.8 87.7 22.8 87.7 22.8 87.7 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 24.0 22.8 87.7 25.	œ	~	~	~	~	~	9	е		9				•	•	•	4		4	σ	•	_	4	9
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ALIGNMENTS

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Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; PCR primer; ss.
                                                                                                                                                                                                                                                                                                             New universal primers, mcb 398 and mcb 869, capable of amplifying a
                                                                                                                                                                                                                                                                                                                   fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for
                                                                                   Cytochrome b gene universal PCR primer mcb 369 SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                           molecular evidence in forensics.
                     BP.
                                                                                                                                                                                                                                             (COUL ) COUNCIL SCI & IND RES.
                                                                                                                                                                                                     28-MAR-2001; 2001WO-IN000055
                                                                                                                                                                                                                         28-MAR-2001; 2001WO-IN000055
                     ABQ83298 standard; DNA; 26
                                                              (first entry)
                                                                                                                                                                                                                                                                                        WPI; 2003-018945/01.
                                                                                                                                                                                                                                                                    Verma SK, Singh L;
                                                                                                                                                            WO200277278-A1
                                                              18-JAN-2003
                                                                                                                                                                                 03-OCT-2002
                                                                                                                                       Synthetic
                                          ABQ83298;
RESULT 1
           ABQ83298
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(see ABQ83297 and ABQ83298), capable of amplifying a fragment of expodence b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of

Mitochond

The present invention describes universal primers, mcb 398 and mcb 869

Claim 1; Page 116; 128pp; English.

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controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected form the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime to confine the blood of an when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confiuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics
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                           poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court claw, so that human violation of the wildlife resources could be
biological materials such as skin, horns confiscated from animal
555555555555555555555888
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Sequence 26 BP; 4 A; 5 C; 7 G; 10 T; 0 U; 0 Other;

Gaps .; 0 100.0%; Score 26; DB 8; Length 26; 100.0%; Pred. No. 0.025; 0; Indels 0; Mismatches 100.08; Query Match Best Local Similarity 100.0 Matches 26; Conservative ð

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g

ABQ83306 standard; DNA; 472 BP. ABQ83306/c RESULT 2

ABQ83306;

Mitochondrial cytochrome b gene sequence SEQ ID NO:11.

(first entry)

18-JAN-2003

Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds.

Unidentified.

WO200277278-A1

03-OCT-2002.

28-MAR-2001; 2001WO-IN000055.

28-MAR-2001; 2001WO-IN000055

& IND RES (COUL) COUNCIL SCI

Singh L; Verma SK,

WPI; 2003-018945/01.

New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.

Example 1; Page 28-57; 128pp; English.

The present invention describes universal primers, mcb 398 and mcb 869 (see AB083297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identitity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of

The present invention describes universal primers, mcb 398 and mcb 869 (see ABQ83297 and ABQ83298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the

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biological materials such as skin, horns confiscated from animal

components, if it is that of an endangered species, for the purpose of

molecular evidence of animal hunting and related crime in the court of

law, so that human violation of the wildlife resources could be

controlled, to have an idea of the geographical location of the

commitment of wildlife crime based on the cytochrome b gene haplotype of

commitment of wildlife orime based on the cytochrome b gene haplotype of

commitment of wildlife orime based on the cytochrome b gene haplotype of

commitment of wildlife orime based on the cytochrome b gene haplotype of

cortification, by the food fortification agencies, to provide a universal

controlled to a crime related to offenses such as murder and rape,

in order to establish the origin of blood or blood stains collected

converted to a criminals intentionally spread the blood of an

animal at the scene of the crime to confuse the crime investigators and

converted to a commercial molecular kit and DNA chips based applications

for wildlife identification in forensics. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                a mitochondrial cytochrome b gene sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 26; DB 8; Length 472; 100.0%; Pred. No. 0.034; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrial cytochrome b gene sequence SEQ ID NO:12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ83307 standard; DNA; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ83307/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal beconders, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime in order to establish the origin of blood at the scene of the crime
                                                                                                                                                                                                                                                                                                                                                                                                              when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents a mitochondrial cytochrome b gene sequence from the present invention
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Score 26; DB 8; Length 472; Pred. No. 0.034; Sequence 472 BP; 141 A; 153 C; 66 G; 112 T; 0 U; 0 Other; 0; Indels 0; Mismatches 1 CCTCCTAGTTTGTTAGGGATTGATCG 26 100.0%; 100.0%; Query Match
Best Local Similarity 100.v

0

Gaps

; 0

472 CCTCCTAGTTTGTTAGGGATTGATCG 447 원 ò

ABX44247 standard; cDNA; 200 BP 21-FEB-2003 ABX44247; RESULT 4
ABX44247/c
ID ABX442

(first entry)

Bovine EST associated with lactation/muscle/fat deposition #9412.

Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

Bos Taurus.

US2002137139-A1.

26-SEP-2002

24-SEP-2001; 2001US-00960352.

12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902.

(BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.

TAO N.

WARREN W C. (TAON/)

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. useful for genome mapping, gene

Warren WC;

Tao N,

Mathialagan N,

Syatt JC,

WPI; 2003-110599/10.

Claim 2; SEQ ID NO 9412; 245pp; English.

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from

cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are idlined to a promoter and a3' non-translated sequence that acid linked to a promoter and a3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle or genemically improving cattle. The present sequence is one of the present sequence was not shown in the specification but was obtained in constructs for genemic form the USPTO web site: ö New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle. Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. Gaps Bovine EST associated with lactation/muscle/fat deposition #3962. .; 0 Score 24.4; DB 8; Length 200; Pred. No. 0.17; 0; Mismatches 1; Indels (Sequence 200 BP; 62 A; 66 C; 28 G; 44 T; 0 U; 0 Other; segdata.uspto.gov/sequence.html?DocID=20020137139 Warren WC; 1 CCTCCTAGTTTGTTAGGGATTGATCG 26 36 CCTCCTAGTTTGGGGATTGATCG 11 Tao N, ABX38797 standard; cDNA; 235 BP. 99US-0115707P. 12-JAN-1999; 99US-0115707P. 24-SEP-2001; 2001US-00960352 Query Match
Best Local Similarity 96.2%;
Matches 25; Conservative Mathialagan N, (first entry) (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
(TAON/) TAO N. PI; 2003-110599/10. (WARR/) WARREN W C. US2002137139-A1. 20-FEB-2003 26-SEP-2002. 30s Taurus Byatt JC, ABX38797; RESULT 5 ABX38797/c ò

WPI; 2003-110599/10.

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from a cattle LMFD nucleic acid can specifically Mybridise to a second nucleic acid molecule comprising any of 15:12 nuclectide sequences.

The inventor as ABX34836-ABX49947, or complements of them. Also included are complements as a partial and a sequence of the nucleic acid comprising an uncleic acid comprising an LMPD nucleic acid linked to a promoter and a 3, non-translated sequence that comprising in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and comprising a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue to make the molecule. The LMFD nucleic acid is used for the detection of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for complementary nucleic acid permits the detection of constructs for use in cattle gene expression, or complementary proposed mapping, gene identification and analysis, cattle complementary proposed to the complementary sequence is one of the complementary sequence was not shown in the sequence eight one of the present sequence is one of the complement sequence was not shown in the specification but was obtained in a larger of the supermited for make them the molecules is a present and the sequence was not shown in the specification but was obtained in a larger of the supermited and the sequence of the supermited and the sequence as and the supermited and the
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Pred. No. 0.18;
0; Mismatches 1; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               segdata.uspto.gov/sequence.html?DocID=20020137139
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                                        Claim 2; SEQ ID NO 3962; 245pp; English.
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11-JAN-2000; 2000US-00480902.
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(MATH/) MATHIALAGAN N.
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(TAON/) TAO N.
(WARR/) WARREN W C.
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if it are associated to a promoter and a3 non-translated sequence that concluded to a promoter and a3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mina modecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle tris useful for genome mapping, gene identification and analysis, cattle breading, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The molecule tage acide acide is the confidence become mapping or the molecule or acide acide acide the confidence become mapping or the molecule or acide acide acide acide the complementary nucleic acide is used for the detection of constructs for use in cattle gene expression, or for genetically improving cattle. The molecule tage acide acide acide the confidence acide aci
                                                                        New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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0; Mismatches
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                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 5417; 245pp; English.
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ID ABX38833 standard; cDNA; 331 BP.
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11-JAN-2000; 2000US-00480902.
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nes 25; Conservative
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34815-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and 3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3 non-translated sequence cell or tissue comprising a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the list bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
                                                                                                                                                   New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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muscle deposition; fat deposition; genome mapping; gene identification;
gene analysis; cattle breeding.
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(TAON/) TAO N.
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cartie, and the LMFD micret actu can specifically withints to a cartie, and molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' annon-translated sequence that functions in the cell to cause termination of transcription and addition of polyademylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid where the complementary nucleic acid is predictive of the complementary nucleic acid is used for detecting the level or pattern of a molecule in a bovine cell or tissue. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the contract of the present sequence is one of the contract of the contract of the present sequence is one of the contract of t
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                                                                                                                                                                                                                                                                                                      New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
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12-JAN-1999; 99US-0115707P.
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                                                                                                                                                                                                           Mathialagan N,
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                                                                                                        z
                                                                           (BYAT/) BYATT J C. (MATH/) MATHIALAGAN
                                                                                                                                                                                                                                                              WPI; 2003-110599/10.
                                                                                                                                                        (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                   TAO N.
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                                                                                                                                                                                                           3yatt JC,
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                                                                                                     (MATH/)
(TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
ABX44048/c
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US2002137139-A1

gene analysis; cattle breeding.

24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902.

US2002137139-A1 26-SEP-2002.

Bos Taurus.

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMPD), derived from cattle, and the LMFD nucleic acid can specifically bybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are if (1) a transformed call having a nucleic acid comprising an LMFD nucleic caid linked to a promoter and a 3 non- translated sequence that conformed call to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 1512 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid molecule obtained from the bovine cell or tissue, the detection of the complementary nucleic acid germits the detection of the molecule. The LMFD nucleic acid, where the detection of the molecule. The LMFD nucleic acid, such the complementary nucleic acid is used for the detection of constructs for use in cattle gene expression, or determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle for genetically improving cattle. The present sequence is one of the 1512 bovine LMFD EST (expressed sequence tag) nucleic acids note: The present sequence was not shown in the specification but was obtained in alert nor pattern of sequence was not shown in the specification but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                              New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 416 BP; 138 A; 132 C; 57 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              segdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                               Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ectronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 9213; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTCCTAGTTTGTTAGGGATTGATCG
                                                                                                                                                                                                                                                                               Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX47842 standard; cDNA; 417 BP
                                                                                                     12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%;
                                                             24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                                                                             Byatt JC, Mathialagan N,
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Best Local Similarity 96.2
Matches 25; Conservative
                                                                                                                                                                  (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                           TAO N.
WARREN W C.
                                                                                                                                                                                                                                                                                                                        WPI; 2003-110599/10
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                  26-SEP-2002.
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                                                                                                                                                                                                             (TAON/)
(WARR/)
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 1512 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a3 non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprementary nucleic acid molecule obtained from the bovine cell or complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is used for the detection of the molecule. The LMFD nucleic acid is used for level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle tria useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the content of the complement expenses and content of the content of constructs for use in cattle gene expression, or content of the content

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Tao N,

Byatt JC, Mathialagan N,

WPI; 2003-110599/10.

(BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.

(TAON/) TAO N. (WARR/) WARREN W C.

Claim 2; SEQ ID NO 13007; 245pp; English.

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0
                                                                                                                                                                                                                                                                                                                     93.8%; Score 24.4; DB 8; Length 417; 96.2%; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                           Sequence 417 BP; 137 A; 138 C; 53 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      152 ccrccracrrcrrcrrccaccarrcarcc 127
                                                                                                                                                                                                                                                                                                                                            56
                                                                                                                                                                                                                                                                                                                                            1 CCTCCTAGTTTGTTAGGGATTGATCG
                                                                                                                                                                                                                                                                                                                                                                                  ABX37167 standard; cDNA; 419
                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                           Local Similarity 96.2
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ABX37167;
                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                 Matches
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present sequence was not shown in the specification but was obtained in

à 엄 ABX43592 standard; cDNA; 448 BP.

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New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                       Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
       Bovine EST associated with lactation/muscle/fat deposition #2332
                                                                                                                                                                                                                Tao N, Warren WC;
                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 2332; 245pp; English.
                                                                                                                                        12-JAN-1999; 99US-0115707P
11-JAN-2000; 2000US-00480902
                                                                                                                     24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence was not
                                                                                                                                                                 (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                    WPI; 2003-110599/10.
                                                                                                                                                                                              WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for genetically
15112 bovine LM
                                                                                 US2002137139-A1
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                                                                                                    26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electronic
                                                                Bos Taurus.
                                                                                                                                                                                     (TAON/)
(WARR/)
%XCCCCCCCCCCCCCCCCCCCCCCCCX
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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are : (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and cit losue comprising: (a) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid sequences or its complement or fragment) with a complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or shown in the specification but was obtained in pretically improving cattle. The present sequence is one of the bovine LMFD EST (expressed sequence tag) nucleic acids. Note: 7 segdata.uspto.gov/sequence.html?DocID=20020137139 format from the USPTO web sit

93.8%; Score 24.4; DB 8; Length 419; 96.2%; Pred. No. 0.19; Sequence 419 BP; 123 A; 141 C; 53 G; 102 T; 0 U; 0 Other; Query Match

RESULT 12 ABX43592/c

Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. 3ovine EST associated with lactation/muscle/fat deposition #8757. (first entry) US2002137139-A1 26-SEP-2002. 21-FEB-2003 Bos Taurus. ABX43592;

24-SEP-2001; 2001US-00960352. 12-JAN-1999; 99US-0115707P. 11-JAN-2000; 2000US-00480902. (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. (WARR/) WARREN W C. TAON/)

Tao N, Warren WC; Byatt JC, Mathialagan N,

WPI; 2003-110599/10

New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

Claim 2; SEQ ID NO 8757; 245pp; English

The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are illused to a promoter and a 3' non- translated sequence that caid linked to a promoter and a 3' non- translated sequence that cfunctions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and complementary nucleic acid sequences or its complement cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and the complementary nucleic acid permits the detection of the molecule, and the complementary nucleic acid molecule obtained from the molecule, and the complementary nucleic acid is predictive of the externing a level or pattern of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. Cell tis useful for genome mapping, gene identification and analysis, cattle complementary proparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs of sequence tag) nucleic acids acids. present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: segdata.uspto.gov/sequence.html?DocID=20020137139

Sequence 448 BP; 131 A; 146 C; 55 G; 116 T; 0 U; 0 Other;

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Gaps

0

Indels

ij

0; Mismatches

Conservative

Best Local Similarity

25;

Matches

.. Match 93.8%; Score 24.4; DB 8; Length 448; Local Similarity 96.2%; Pred. No. 0.19; les 25; Conservative 0; Mismatches 1; Indels (Query Match Matches

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Gaps

1 CCTCCTAGTTTGTTAGGGATTGATCG 26

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o,

Pred.

96.2%;

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lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49347, or complements of them. Also included are 1 (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and of polyadenylated ribonucleotides to a' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the complementary nucleic acid sequences or its complementary nucleic acid permits the detection of the molecule. The LMFD nucleic acid is used for determining a level or pattern of the molecule in a bovine cell or tissue.

The detection of the complementary nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. The LMFD second analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the constructs for the constructs for the constructs for genetically income.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.
                                                                                                                                                                                                                                                                                                                         Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                          Bovine EST associated with lactation/muscle/fat deposition #1158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tao N, Warren WC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 1158; 245pp; English
404 CCTCCTAGTTTGTTGGGGATTGATCG 379
                                                                                                                          ABX35993 standard; cDNA; 469 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JAN-1999; 99US-0115707P.
11-JAN-2000; 2000US-00480902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-2001; 2001US-00960352
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Byatt JC, Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-110599/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WARR/) WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002137139-A1.
                                                                                                                                                                                                                           20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                             Bos Taurus
                                                                                                                                                                            ABX35993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATH/)
(TAON/)
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15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in Sequence 469 BP; 138 A; 160 C; 53 G; 117 T; 0 U; 1 Other; seqdata.uspto.gov/sequence.html?DocID=20020137139 lectronic format from the USPTO web site:

The present into the control of any animal species in polymerase chain med soy of see AB083297 and AB083299. Capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction of the identification of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal confiscated animal hunting and related from animal concentration of animal hunting and related crime in the court of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal prime invented, to detect the adulteration of animal meat in food products for the purpose of food adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as marder and rape, the prime it sould be added to be comed an interval and its collected from the scene of the crime related to offenses such as marder and rape, the prime is some of the crime related to offense such as marder and rape, the collected to offense such as marder and rape, the collected to offense such as marder and rape, the collected to offense such as marder and rape. The present sequence represents converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represent when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be present invention describes universal primers, mcb 398 and mcb 869 for wildlife identification in forensics. The present sequence repress a mitochondrial cytochrome b gene sequence from the present invention Gaps New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics. Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds. 6 Indels Mitochondrial cytochrome b gene sequence SEQ ID NO:19. 1, 0; Mismatches 378 cerectasirierresesarreares 353 56 Example 1; Page 28-57; 128pp; English. ABQ83314 standard; DNA; 472 BP (COUL) COUNCIL SCI & IND RES 28-MAR-2001; 2001WO-IN000055. 28-MAR-2001; 2001WO-IN000055. (first entry) Best Local Similarity 96.28 Matches 25; Conservative WPI; 2003-018945/01. Verma SK, Singh L; WO200277278-A1 18-JAN-2003 Unidentified 03-OCT-2002. ABQ83314; Matches RESULT 14 ABQ83314/ The ਨੋ g

Sequence 472 BP; 145 A; 151 C; 66 G; 110 T; 0 U; 0 Other;

DB 8; Length 469; 93.8%; Score 24.4;

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                                               Gaps
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0
Query Match 93.8%; Score 24.4; DB 8; Length 472; Best Local Similarity 96.2%; Pred. No. 0.19; Matches 25; Conservative 0; Mismatches 1; Indels
                                                                                            1 CCTCCTAGTTTGTTAGGGATTGATCG 26
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472 cerecraciristrassaarrsarcs 447

RESULT 15 ABQ83313,

ABQ83313 standard; DNA; 472

ABQ83313;

(first entry) 18-JAN-2003 Mitochondrial cytochrome b gene sequence SEQ ID NO:18.

Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds. Mitochondrial

Unidentified.

WO200277278-A1.

03-OCT-2002.

28-MAR-2001; 2001WO-IN000055.

28-MAR-2001; 2001WO-IN000055.

(COUL) COUNCIL SCI & IND RES

Singh L; Verma SK,

WPI; 2003-018945/01

New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics

Example 1; Page 28-57; 128pp; English.

The present invention describes universal primars, mco 398 and mcb 899 (see AB083297) and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction of unknown origin at species and sub-species level. Also described is a method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the crime with the criminal beyond a reasonable doubt, to establish the crime with the crime till it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related from animal controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the commitment of animal meat in food products for the purpose of food fortification agencies, to provide a universal certhique for detection of the origin of blood or blood stains collected from in order to establish the origin of blood found at the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the crime investigators and formerial at the scene of the crime to confuse the crime investigators and formered to a commercial molecular kit and DNA chips based applications of printed to a commercial molecular kit and DNA chips based applications of printed to a commercial molecular kit and DNA chips based applications of printed to the printed to a commercial molecular for the present sequence of printed to a commercial molecular for the printed printed printed for the printed printed The present invention describes universal primers, mcb 398 and mcb 869 a mitochondrial cytochrome b gene sequence from the present invention

Sequence 472 BP; 147 A; 145 C; 63 G; 117 T; 0 U; 0 Other;

ô Gaps .; 0 Length 472; Indels Score 24.4; DB 8; Pred. No. 0.19; 0; Mismatches ch 93.8%; 1 Similarity 96.2%; 25; Conservative (Query Match Best Local Similarity Matches 25; Conserv

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November 17, 2004, 00:09:11

Search completed: Noveml Job time: 45.4054 secs

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CB066285 4010439 B
AU277825 AU277825
BM430528 IDW035F3.
BE589920 196607 BA
BE589920 196607 BA
BE589920 196607 BA
BM433056 ILEJ9D3.a
BP112175 BP112175
BP412175 BP112175
BP412175 BP112175
BP413038 IUEJ9B6.a
AV613710 AV613710
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BE488891 170238 BA
CB220057 IAbolGG09
CB2240555 1095 MARC
BF429555 1096 MARC
CB2249532 1068 MARC
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CB22555 1068 MARC
                                                                       November 16, 2004, 22:24:28; Search time 343.642 Seconds (without alignments) 2650.992 Million cell updates/sec
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                                                                                                                                                                                                                                         65645750
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                              32822875 seqs, 18219865908 residues
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Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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CB060285
CF6175703
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gb_est4:;
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CN432453 BE0200010 BM480699 531379 MA CN822416 Oa splbn BF604803 270971 MA BM430200 1Du031D6. BP110300 BP110300 CP931047 CF06-R BM432066 1JED16410 BM445456 1JED16410 CM2231647 1ED255C9 CB220685 1APD255C08 CB220685 1APD255C08 CB221081 1L121H5 B BM434623 1RT11A03 BF65223 3777 1ABC31M6 CB221081 1AbO30A09 CB221081 1AbO30A09 CB221081 1AbO30A09 CB222631 1IL130B01 BP110116 BP110116	SEL	Abomasum #1 library Bos taurus cDNA, mRNA 509 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Ore,S.S. iling of the Bovine Gastrointestinal Tract Moore tory ### AFNS, U of A, Edmonton, AB, T6G 2P5, Canada ### AFNS, U of A, Edmonton,		DB 6; Length 130; 0.89; hes 0; Indels 0; Gaps 0;
25 100.0 456 7 CN432453 25 100.0 462 4 BM480699 25 100.0 467 7 CN822416 25 100.0 479 4 BM43202 25 100.0 479 5 BP110300 25 100.0 479 5 BP110330 25 100.0 482 7 CF931047 25 100.0 484 6 CB220695 25 100.0 485 6 CB221041 25 100.0 489 6 CB221941 25 100.0 489 6 CB221941 25 100.0 489 6 CB221081 25 100.0 489 6 CB221081 25 100.0 489 6 CB221081 25 100.0 489 6 CB221081 25 100.0 499 6 CB221081	ALIGNMENTS	CB219995 130 bp mRNA 1Abol0D11 Bos taurus Abomasum #1 library sequence. CB219995.1 GI:28290509 EST. Bos taurus (cow) Mammalia; Eutheria; Cetartiodactyla; Rum Bovinae; Bos. 1 (bases 1 to 130) Hansen, C., Fu, A., Meng, Y., Li, C., Okine; Gordon, P.M.K. and Noore, S.S. Gons Expression Profiling of the Bovine; Gontact: Dr. Stephen Moore Beef Genomics Laboratory Dept of AFNS, University of Alberta 10 Ag1/For. Dept of AFNS, U of A, Edmon Tel: 780 492 4265 Eax: 780 492 4265 Eax: 780 492 4265 Eax: 780 492 4265 Eax: 780 492 4265 Location/Qualifiers 1. 130 /organism="Bos taurus" /db xref="taxon:9913" /tissue_type="mRnA" /db xref="taxon:9913" /tissue_type="mRnA" /db Aref="taxon:9913" /tissue_type="mRnA" /db host="Yung adult" /dab_host="Yung adult" /dab_host="Yung adult" /dab_host="Yung adult" /dab_host="Xung adult" /dab_host="Yung adult" /dab_host="Yung adult" /dab_host="Xung adult" /dab_host="Yung adult	t	th 100.0%; Score 25; D Similarity 100.0%; Pred. No. 0. 25; Conservative 0; Mismatches
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1 TACCATGAGGACAAATATCATTCTG 25

EST 01-OCT-2003

Dierens, L.

RESULT 2 CB060285/c

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/dev_stage="Young_Adult"
/lab_hos=="XIJ-BlueWRF'strain"
/lab_hos=="XIJ-BlueWRF'strain"
/loon= lib==Bos taurus muscle cDNA library"
/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1:
BCORI, Site_2: Xho I; Library made from skeletal muscle of a 14 month Old Angus steer."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU277825 Cloned bovine fetus cDNA Bos taurus cDNA clone fetus377E11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dr Sigrid Lehnert
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Bloscience Precinct, University of Queensland,
306 Carmody Road St.Lucia QLD Australia
11: 07 3214 2445
Fax: 07 3214 2485
Bmail: Sigrid.Lehnert@csiro.au
Plate: 12 row: H column: 05.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         ranscription profiling of bovine skeletal muscle and subcutaneous
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                      328 bp mRNA linear EST 01-OCT.
CES014188 Bos taurus muscle cDNA library Bos taurus cDNA clone
CCL013263 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 328)
Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S.,
and Lehnert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 7; Length 328; Pred. No. 0.99;
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Unpublished (2002)
Contact: Masahito Oishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="Longissimus dorsi muscle"
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100.0%; Pred. No. ...
0; Mismatches

    .328
    /organism="Bos taurus"

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/strain="Angus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                               Bos taurus (cow)
Bos taurus
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JOURNAL
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KEYWORDS
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RESULT 3
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/ site_2: HincII; This mammary-derived cDNA library was
Created as part of a collaborative project between the ARS
Gene Evaluation and Mapping laboratory and the EMBRAPA
Bairy Cattle Research Center under the sponsorship of
Bairy Cattle Research Center under the sponsorship of
Sample from cow AMI, samples 2, 4, and 5 extracted on
3/27/02, RT with Superscript II at 37 deg C annealing
temperature, PCR with 16-mers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                 CB060285 315 bp mRNA linear EST 17-JAN-2003 4010439 BARC-EMBRAPA 326BOV Bos indicus cDNA clone 326BOV_1005
                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 315)

da Mota, A.F., Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K.,
da Mocd, D.L., Capuco, A.V., Brito, M.A.P., Martinez, M.L., Connor, B.E.,
Machado, M.A. and Coutinho, L.L.
Construction and Characterization of CDNA Libraries Generated from
Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '' -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 12 PCR PRimers
                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
Contact: Adilson F. da Mota
Contact: Adilson F. da Mota
Gene Bvaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources Institute
Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA
Fax: 3015048456
Exx: 3015048414
Exx: 3015048414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol type="mRNA"
/strain="Brazilian Dairy Gir"
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Plate: 1 row: 0 column: 05
Seq primer: GTTTCCCAGTCACCACCACCACGACGTG
High quality sequence stop: 315.
Location/Qualifiers
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'organism="Bos indicus"
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  52 TACCATGAGGACAAATATCATTCTG 76
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                                                                                                                                                                                      Unknown, mRNA sequence.
CB060285
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Bos indicus
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source

ORIGIN

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FEATURES

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Gaps

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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Balgo. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8414
Fax: 301 504 8414
Email: tade@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="BARC 5BOV"
/roto="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."
                                                                                   EST 27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 27-MAR-2003
                                                                                                                                                                                                                                                                                               1 (bases 1 to 398)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (cow)
Bos taurus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                        Bos taurus (cow)
Bos taurus Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                   3589920 398 bp mRNA linear 196607 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
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Mamm. Genome 13 (7), 373-379 (2002)
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PCR PRimers
FORWARD: AGGAAACAGCTATGACGAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 118 row: F column: 21
Seq primer: ATTAGGTGACACTATGG.
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/organism="Bos taurus"
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1 (bases 1 to 398)
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BE589920
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Beef Genomics Laborators of Alberta
Dept of AFNS, University of Alberta
Alto Agriffor, Dept of AFNS, U of A, Edmonton, AB, T6G 2PS, Canada
Tel: 780 492 0169
Fax: 780 492 4265
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1Du035F3.abl Bos taurus Duodenum #1 library Bos taurus CDNA, mRNA
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector: Uni-2ZAPXR;
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                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; Length 338; llarity 100.0%; Pred. No. 0.99; Conservative 0; Mismatches 0; Indels
Graduate School of Agriculture
Kyoto University
Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6331
Fax: 81-75-753-634
Email: olshi@jkans.jkans.kais.kyoto-u.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: stephen.moore@ualberta.ca
Insert Length: 361 Std Error: 0.00
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                                                                                                                                                                        /organism="Bos taurus"
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BM430528.1 GI:18452250
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This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuba@affrc.go.jp This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and Technology.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,
Takahashi,T., Imal,K., Hirasawa,A., Shiojima,S., Ikawa,H.,
Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray
Mol. Reprod. Dev. 65 (1), 9-18 (2003)
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/note="Organ: Intestine/jejunum; Vector: Uni-2ZAPXR;
Site_1: EcoRI; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Gozoh Tsujimoto
Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev stage="adult"
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ilarity 100.0%; Pred. No. 1;
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                          organism="Bos"
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Fax: 81-3-3149-1252
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/lab host="DH10B"
/lab host="DH10B"
/loore lib="BARC SBOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
                                                                                                                                                                                                                                                                                                      Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
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Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agriffer, Post olegt of ARNS, U of A, Edmonton, AB, TGG 2P5, Canada
Tel: 780 492 4165
Fax: 780 492 4265
                                                                    Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM433056 408 bp mRNA linear EST 31-JAN-2
1JEJ9D3.ab1 Bos taurus Jejunum #1 library Bos taurus CDNA, mRNA
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100.0%; Pred. No. 1;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                 Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8414
Fax: 301 504 8414
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Insert Length: 408 Std Error: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Bos taurus"
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Plate: 34 row: I column: 18
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'mol_type="mRNA"
'db_xref="taxon:9913"
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BP110134 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone ORCS10131 5', mRNA sequence.
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This work was performed to collaborate with Developmental Biology
This work was performed to collaborate with Developmental Biology
Department, National Institute of Agobiological Sciences. Address:
2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
81-29-838-8633 e-mail: kazuha@affrc.go.jp
This work was funded by Organized Research Combination System
(ORCS) project of Ministry of Education, Culture, Sports, Science
and Technology.
Location/Qualifiers
               Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 414 Std Error: 0.00
                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/note="Organ: Omasum; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H.,
Ishiwata,H., Imai,K., Hirasawa,A., Shiojima,S., Ikawa,H.,
Suzuki,Y., Tsujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
Characterization of gene expression profiles in early bovine pregnancy using a custom cDNA microarray
MOL. Reprod. Dev. 65 (1), 9-18 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Molecular, Cell Pharmacology
National Research Institute for Child Health and Development
3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
Tel: 81-3-3149-1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 25; DB 6; Length 414; Best Local Similarity 100.0%; Pred. No. 1;
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                                                                                                                                                                                                                                            1. .414
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1JEJ9B6.abl Bos taurus Jejunum #1 library Bos taurus cDNA, mRNA
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Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
Gordon,P.M.K. and Moore,S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of ARNS, University of Alberta
HI AgrifFor, Dept of ARNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
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site_1: EcoRI; Site_2: Xho I
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IOM28B03 Bos taurus Omasum #1 library Bos taurus CDNA, mRNA
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Insert Length: 413 Std Error:
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                                             386 raccardaddacaaararcarrcrg 410
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/db_xref="taxon:9913"
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Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H. and Sugimoto, Y. and Sugimoto, Y. Establishment of a high throughput EST sequencing system using poly (A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 436) and add A.E., Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Wood, D.L., Capuco, A.V., Brito, M.A.P., Martinez, M.L., Connor, E.E., Machado, M.A. and Coutinho, L.L.

Construction and Characterization of cDNA Libraries Generated from Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos indicus) Cattle
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site 1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                              Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 1; Length 432; ilarity 100.0%; Pred. No. 1; Conservative 0; Mismatches 0; Indels
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Contact: Adilson F. da Mota
Contact: Adilson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources Institute
Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshikazu Sugimoto
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AV663157.1 GI:9922187
                                                                                                                                                         (bases 1 to 432)
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                                           Bos taurus (cow)
Bos taurus
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AV613710 Bos taurus adipocyte cell line Bos taurus cDNA clone E000009001 5', mRNA sequence.
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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
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3', mRNA sequence.
AV663157
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Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Bos taurus adipocyte cell line"
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was deleted from a Not1 site"
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Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Fat: 81-248-25-5725
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0
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.larity 100.0%; Pred. No. 1;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="an adipocyte cell line"
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                                                                                                                                                                                                                                              373 TACCATGAGGACAAATATCATTCTG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 TACCATGAGGACAAATATCATTCTG 402
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Location/Qualifiers
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clone="ORCS10131"
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AV613710.1 GI:9749380
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REFERENCE AUTHORS

TITLE

COMMENT

FEATURES

DRIGIN

KEYWORDS

RESULT 14

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/ ceal type="parenchyma" / tissue_type="parenchyma" / tissue_type="parenchyma" / ceal type="parenchyma" / dea' fiasue_type="parenchyma" / dea' fiasue_type="parenchyma" / dab_host="DH5alpha" / dabo=lib="BaRC-EMBRAPA 326BoV" / dabo=lib="baRC-EMBRAPA 326BoV" / note="Organ: mammary Vector: pUC 118; Site_1: HincII; / note="Organ: mammary; Vector: pUC 118; Site_1: HincII; / note="Organ: mammary; Vector: pUC 118; Site_1: HincII; / note="Organ: mammary; Vector: puc note on Site_2: HincII; / note="Organ: mammary; Vector: note on sample from cow AMI, samples 2, 4, and 5 extracted on 3/27/02, RT with Superscript II at 37 deg C annealing temperature, pCR with 16-mers:"
FEATURES
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342 TACCATGAGGACAAATATCATTCTG 366 1 TACCATGAGGACAAATATCATTCTG 25 ð g

Query Match
100.0%; Score 25; DB 6; Length 436;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels

ORIGIN

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Search completed: November 17, 2004, 02:10:47 Job time : 349.642 secs

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Sequence 14288, A
Sequence 6557, Ap
Sequence 6350, Ap
Sequence 7247, Ap
Sequence 1396, Ap
Sequence 12218, A
Sequence 7805, Ap
Sequence 4672, Ap
Sequence 9374, Ap
Sequence 9374, Ap
                                                                                                               November 16, 2004, 23:47:45; Search time 37.2849 Seconds (without alignments) 3621.431 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-960-352-6557
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US-09-960-352-1347
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US-09-960-352-4678
US-09-960-352-7414
US-09-960-352-84988
US-09-960-352-84988
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Maximum Match 100%
Listing first 45 summaries
                                                                              - nucleic search, using sw model
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25
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ALIGNMENTS

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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 34-BOVMS1-002-Q1-E1-A6
US-09-960-352-7805
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            APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE REPERENCE: 16511.006/377-21(10298)C
CURRENT APPLICATION NUMBER: US/09/966,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6557
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.066/37-21 (10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6350
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Tao, Nembing
APPLICANT: Tao, Nembing
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
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                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Bos taurus
. OTHER INFORMATION: Clone ID: 28-LIB34-007-Q1-E1-G7
US-09-960-352-6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
OGANTSM: Bos taurus
OTHER INFORMATION: Clone ID: 27-LIB34-033-Q1-E1-G3
US-09-960-352-6350
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
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Matches 25, Conservative
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Matches 25; Conserv
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US-09-960-352-6350
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Sequence 1396, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wasley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathiadagan, Nugappan
APPLICANT: Mathiadagan, Nugappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 1396
LENGTH: 388
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Sequence 7805, Application US/09960352

Patent No. US2002013713941

GENERAL INFORMATION:
APPLICANT: Warren, Weeley C.
APPLICANT: Byat, John C.
CURRENT PAPLICANTION: WUSCLE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: WUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICANTION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7805

SEQ ID NO 7805
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TYPE: DNA CRGANISM: Bos taurus CORGANISM: Bos taurus COTHER INFORMATION: Clone ID: 31-LIB34-008-Q1-E1-H11 US-09-960-352-7247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (44), (60)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 07-BOVMS1-018-Q1-E1-B3
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RESULT 10
US-09-960-352-9374
Squence 9374, Application US/09960352
Factor No. US20020137133A1
GENERAL INFORMATION:
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: NUCLEIC ACID AND STILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICANTION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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LOCATION: OFFICE at all n locations
OTHER INFORMATION: Unsure at all n locations
OTHER INFORMATION: Clone ID: 32-LIB3057-021-Q1-K1-H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-LIB34-028-Q1-E1-B12
US-09-960-352-9374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatr, John C.
APPLICANT: Mathialagan, Nagappan
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Best Local Similarity 100.
Matches 25; Conservative
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Pacent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathadam, Nagappan
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REPRESENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Tao, Nengbing

APPLICANT: John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.066/37-11 (10208) C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 12218

LENGTH: 402
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                                                                                            DB 9; Length 397;
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OTHER INFORMATION: Clone ID: 20-LIB34-031-Q1-E1-E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-LIB34-007-Q1-E1-E8
US-09-960-352-12218
                                                                        100.0%; Sco...
100.0%; Pred. No. v...
0; Mismatches
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                                                                                            Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Matches 25; Conservative
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Best Local Similarity
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US-09-960-352-4672
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LENGTH: 409
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Matches

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Gaps

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Sequence 11264, Application US/09960352
Sequence 11264, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Weeley C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILLE REFERENCE: 16511.006/37221(10298)C
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11264
LENGTH: 414
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byat, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND PAT DEPOSITION
TITLE OF INVENTION: NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NOWER: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NOS: 15112
                                               100.0%; Score 25; DB 9; Length 413; 100.0%; Pred. No. 0.2; 0; Mismatches 0; Indels
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; ORGANISM: Bos taurus
. OTHER INFORMATION: Clone ID: 48-LIB34-026-Q1-E1-D8
US-09-960-352-11264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-073-Q1-E1-F5
US-09-960-352-5186
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Pred. No. 0.2;
; Mismatches 0
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Machialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10208)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 SEQ ID NOS: 15112
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Patent No. US2002013713941

GENERAL INFORMATION:

APPLICANT: Warren, Weeley C.

APPLICANT: Tao, Nengbing

APPLICANT: Wathialagan, Magappan

TITLE OF INVENTION: MUSCLET ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REPREBENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24
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CRGANISM: Bos taurus
CHER INFORMATION: Clone ID: 36-LIB34-071-Q1-E1-A8
US-09-960-352-8498
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 10-LIB34-017-Q1-E1-C5
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; ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 05-LIB34-063-Q1-E1-B1
US-09-960-352-1120
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 16, 2004, 16:25:24; Search time 769.82 Seconds (without alignments) 3218.578 Million cell updates/sec Run on:

US-09-821-782E-48 Title: Perfect score:

1 taccatgaggacaaatatct.....attcctaacaaactaggagg 472 Sequence:

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Scoring table:

Gapop 10.0 , Gapext 1.0

8269772 hits satisfying chosen parameters: 4134886 segs, 2624710521 residues Fotal number of Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* Database

geneseqn2003cs:* geneseqn2003ds:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn1980s:* geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

SUMMARIES

Description	Abg83296 Antilope		Abg83307 Mitochond	Abq83306 Mitochond	Abg83321 Mitochond	Abg83333 Mitochond	Abq83331 Mitochond	Abg83334 Mitochond	Abg83303 Mitochond	Abg83330 Mitochond	Abg83311 Mitochond	Abg83313 Mitochond	Abg83332 Mitochond	Abg83328 Mitochond	Abg83310 Mitochond	Abq83315 Mitochond	Abq83304 Mitochond	Abg83326 Mitochond	Abq83314 Mitochond	Abq83322 Mitochond	Abg83312 Mitochond
ΠD	ABQ83296	ABQ83308	ABQ83307	ABQ83306	ABQ83321	ABQ83333	ABQ83331	ABQ83334	ABQ83303	ABQ83330	ABQ83311	ABQ83313	ABQ83332	ABQ83328	ABQ83310	ABQ83315	ABQ83304	ABQ83326	ABQ83314	ABQ83322	ABQ83312
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Score	472	392	387.2	384	384	376	374.4	374.4	372.8	372.8	371.8	371.2	371.2	371.2	369.6	369.6	369.6	369.6	368	368	368
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ABQ83337 ABQ83301 ABQ83317 ABO83336	ABQ83320 ABQ83320 ABQ83327	ABQ83309 ABQ83338 ABQ83319 ABQ83305	ABQ83323 ABQ83316 ABQ83340	ABQ83339 ABQ83302 ABQ83329 ABQ83324	ABQB3318 ABQB3325 0 ADD52253 AAZ77492 AACB6457 0 ADBS9175
472 8 472 8 472 8	472 8472 8472 86 872 88	472 472 8 472 8 472	472 472 8 472 8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	472 8 472 8 1144 1 3552 2 599 3
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ALIGNMENTS

Antilope cervicapra mitochondrial cytochrome b gene SEQ ID NO:1. BP. ABQ83296 standard; DNA; 472 (first entry) 18-JAN-2003 ABQ83296; RESULT 1 ABQ83296

á Mitochondrial cytochrome b gene; mitochondrial; cytochrome identification; criminal investigation; animal poaching; Antilope cervicapra; blackbuck; gene; ds.

Antilope cervicapra.

WO200277278-A1.

03-OCT-2002.

28-MAR-2001; 2001WO-IN000055

& IND RES. (COUL) COUNCIL SCI

28-MAR-2001; 2001WO-IN000055.

Verma SK, Singh L;

WPI; 2003-018945/01.

ø New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.

Claim 5; Page 116; 128pp; English.

The present invention describes universal primers, mcb 398 and mcb 869 (see AbQB31297 and ABQ81298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the

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criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal form the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the blood stains collected from the scene of the crime to confuse the method of an animal at the scene of the crime to confuse the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in foremaics. The present sequence represents a specifically claimed Antilope cervicapra (blackbuck) mitochondrial
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(COUL) COUNCIL SCI & IND RES

WPI; 2003-018945/01.

Verma SK,

28-MAR-2001; 2001WO-IN000055 28-MAR-2001; 2001WO-IN000055

WO200277278-A1 Unidentified.

03-OCT-2002

Sequence 472 BP; 146 A; 145 C; 61 G; 120 T; 0 U; 0 Other;

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100.0%; Score 472; DB 8; Length 472; 100.0%; Pred. No. 1.5e-137; ive 0; Mismatches 0; Indels
                                       Matches 472; Conservative
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CAACCCTCACCCGATTTTTCGCTTTCCACTTTATTCTCCCCATTTATCATTACAGCCCTTG 180
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83.1%;
                   Best Local Similarity 89.4
Matches 422; Conservative
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                                                                                                                                                                                                                                                                                                                                   Mitochondrial cytochrome b gene; mitochondrial; cytochrome b_i identification; criminal investigation; animal poaching; gene; ds.
                                                                               ACTICCTATITICCATACGCAAICCTCCGATCCAAITCCTAACAACTAGGAGG 472
                                                                                                                                                                                                                                                                                                 Mitochondrial cytochrome b gene sequence SEQ ID NO:13.
                                                                                                                                                                                         ABQ83308 standard; DNA; 472
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18-JAN-2003

RESULT 2 ABQ83308

240

241 CAGACGCAGACAAAATICCATICCACCCCTACTACACTAICAAAGATAICCTAGGAGCIC 300

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the present invention describes universal primers, mice jusquent of caee AB0813297 and AB083298, capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction cytochrome b gene of any animal species in polymerase chain reaction of unknown origin at species and sub-species level. Also described is a comethod is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the crime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the crime with the crime biological materials such as skin, horns confiscated from animal completes, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of any, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to detect the poached animal identified by the universal primer invented, to detect the controlled, to animal meat in food products for the purpose of fortification, by the food fortification agencies, to provide a universal controlled from the scene of the crime related to offenses such as murder and rape, controlled from at the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood cound at the scene of the crime related to offense such as murder and rape, contrast the crime investigators and formalial at the scene of the crime to confuse the crime investigators and commercial molecular kit and DNA chips based applications converted to a commercial molecular kit and DNA chips based applications and probability in the present from the present services.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
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Pred. No. 1.9e-112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 28-57; 128pp; English.
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the Present Invention describes universal primars, where the present invention describes universal primars, where the proposed strangment of cytochrome b gene of any animal species in polymerase chain reaction (PRR) and revealing the identity of the biological material of any animal of the dendical material of any animal companies. The method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the inciminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal pological materials such as skin, horns confiscated from animal concerns, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of findentification of animal meat in food products for the purpose of model animal meat in food products for the purpose of mindlife measure and the second secon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime when it sounds as if criminals intentionally spread the blood of an
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                                                                                                                      CAGATGCAGATAAAATTCCATTCCACCCCTACTACACCATCAAAGACATCCTAGGCGCCC
                                                                                      TACTATTAATTTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
                                                                                                                                                                                                 CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT
                                                                                                                                                                                                                                                        CAGACAACTACCCCCCCCCAAACCCACTTAATACACCCCCTCACATCAAACCCGAATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome b gene; mitochondrial; cytochrome b; n; criminal investigation; animal poaching; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.
                                                                                                                                                                                                                                                                                                               ACTICCIATITICATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrial cytochrome b gene sequence SEQ ID NO:12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification;
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animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents
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                                                                                                                                                                                                                                                                                                                                       121 CAACCCTTACCCGATTTTTTGCCTTCCACTTCATTCTCCCATTCATCATTGCAGCCCTTG
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                                                                                                                                                                                     1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA
                                                                                                                                                                                                                1 recenteaceacaantarcarrereaceaceacacarcarcarcarrerereaa
                                                                                                                                                                                                                                              TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG
                                                               a mitochondrial cytochrome b gene sequence from the present invention
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                                                                                                                          Length 472;
                                                                                          Sequence 472 BP; 141 A; 153 C; 66 G; 112 T; 0 U; 0 Other;
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                                                                                                                        Score 387.2; DB 8;
Pred. No. 6.1e-111;
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88.8%;
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                                                                                                                                           Similarity
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New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.

Example 1; Page 28-57; 128pp; English.

The present invention describes universal primers, mcb 398 and mcb 869

(See AB083297 and AB083298), capable of amplifying a fragment of
cytochrome b gene of any animal species in polymerase chain reaction
(PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
method for the identification of the animal from a biological sample. The
CC of unknown origin at species and sub-species level. Also described is a
method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
Diological materials such as skin, horns confiscated from animal
CC criminal beyond a reasonable doubt, to establish the identity of
Diological materials such as skin, horns confiscated from animal
CC controlled, to have an idea of the wildlife resources could be
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC fortification, by the food fortification agencies, to provide a universal
CC fortification, by the food fortification agencies, to provide a universal
CC fortification, by the food fortification agencies, to provide a universal
CC fortification, by the crime related to offenses such as murder and rape,
CC fortification, by the crime related to offenses such as murder and rape,
CC fortification of the crime related to offenses such as murder and rape,
CC fortification of the crime related to confuse the crime investigators and
CC forming scientists with human blood, and so that the method can be
CC forming scientists with human blood, and so that the method can be
CC forming the forminal prime in the scene of the crime investigators and
CC forming the forminal prime the scene of the crime investigators and
CC forming the forminal problem and so that the method can be
CC forming the forminal problem and so that the method can be
CC forming the forminal problem and so t converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents mitochondrial cytochrome b gene sequence from the present invention

Length 472; Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other; 81.4%; Score 384; DB 8; L ilarity 88.3%; Pred. No. 6.1e-110; Conservative 0; Mismatches 55; Similarity Query Match Local Best Loca Matches

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TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120 rccchiairirgccacagacciagiagaargaarcrgagggggarrcrcagragacaaag 120 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA 180 CAACCCTTACCCGATTTTTTGCCTTCCACTTCTTCCATTCATCATTGCAGCCCTTG 180 CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAAACAACCCCCACAGGAATCTCAT 240 CCATAGTTCACCTCTTATTCCTCCACGAAACAGGATCTAACAACCCCACAGGAATCTCAT 240 CAGACGCAGACAAAATTCCATTCCACCCCTACTACATATCAAAGATATCCTAGGAGCTC 300 CAGACGCAGATAAAATCCCATTCCACCCTACTATACAATCAAGGACATTCTAGGCGCCC 300 CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420 420 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC 360 TATTACTAATCCTAGCCCTCATACTACTACTATTCGCACCCGACCTGCTCGGAGACC 360 9 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTTCAGCAA 1 reccardadeacaararcarrereagegeaacaercarcarcaarcrecrereageaa Gaps ; 55; Indels 417; 241 61 61 121 121 181 181 241 301 361 361 301

The present invention describes universal primers, mcb 398 and mcb 869 (see ABQ83297 and ABQ83298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction.

C (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification to establish the orime with the criminal beyond a reasonable doubt, to establish the orime with the criminal beyond a reasonable doubt, to establish the orime with the polopical materials such as skin, horns confiscated from animal confidence of animal hunting and related crime in the court of poachers, if it is that of an endangered species, for the purpose of concolled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the controlled, to detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood for blood as murder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal and so that the method can be contained to the crime to confuse the related to the crime to confuse the page. New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for identification; criminal investigation; animal poaching; gene; ds. Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; Mitochondrial cytochrome b gene sequence SEQ ID NO:26. Example 1; Page 28-57; 128pp; English. molecular evidence in forensics. ABQ83321 standard; DNA; 472 BP (COUL) COUNCIL SCI & IND RES 28-MAR-2001; 2001WO-IN000055. 28-MAR-2001; 2001WO-IN000055 WPI; 2003-018945/01. SK, Singh L; WO200277278-A1 18-JAN-2003 Unidentified, establishing 03-OCT-2002. ABQ83321; Verma ABQ83321

٠, Sequence 472 BP; 144 A; 154 C; 62 G; 112 T; 0 U; 0 Other; 81.4%; Score 384; DB 8; I 88.3%; Pred. No. 6.1e-110; 0; Mismatches Conservative Query Match Best Local Similarity 417;

or wildlife identification in forensics. The present sequence represents mitochondrial cytochrome b gene sequence from the present invention

converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents

09 9 TACCATGAGGACAATATCTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA

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ATTICCTATTIGCATATGCAATCCTACGATCACTCATCATCCCTAACAAACTAGGAGG 472 ACTICCIATITGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472

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                                                                                                                                       241 CAGACACAGACAAAATCCCATTTCACCCTTACTACACCCTTAAAAGATATCCTAGGGGCCA
ccaccicaccesaricirescerrecacrirarecienteareareareageeres
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                                                                                                                                                                        TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
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                                                                                                    ccaractactactrorrectedadacaggarccaacaataccacaggaattccar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for
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                                                                                                                                                                                                                                                                    ACTICCIATITGCATACGCAATCCICCGATCAATTCCTAACAAACTAGGAGG 472
                                                                                                                                                                                                                                                                                sequence SEQ ID NO:38
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criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of any so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food adulteration of animal meat in food products for the purpose of food fortification primer invented, to detect the fortification of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 472 BP; 141 A; 153 C; 60 G; 118 T; 0 U; 0 Other;
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Best Local Similarity 87.33
Matches 412; Conservative
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Unidentified

(see AB083297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the

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The present introlled ubsolities universal primers, mice just and mice by the present interpresent interpresent interpresent interpresent and sub-species in polymerase chain reaction of cytochrome b gene of any animal species in polymerase chain reaction of unknown origin at species and sub-species lavel. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of concentral evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the poached animal identified by the universal primer invented, to detect the committen of animal meat in food products for the purpose of fortification, by the food fortification agencies, to provide a universal certhique for detection of the origin of blood dor biod stains collected from the scene of the crime related to offense such as murder and rape, in order to establish the origin of blood found at the scene of the crime animal at the scene of the crime the crime the crime the crime animal at the scene of the crime animal at the crime the crime the crime the crime the crime animal at the crime of the crime the crime the crime the crime animal at the crime animal at the crime animal at the crime animal at the crime crime the cr
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                                                                                                                                                                                                                                                (COUL ) COUNCIL SCI & IND RES
                                                                                                                                     28-MAR-2001; 2001WO-IN000055.
                                                                                                                                                                                            28-MAR-2001; 2001WO-IN000055.
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420 241 CAGACACGGACAAAATCCCATTCCACCCTACTATACAATCAAAGACATTCTAGGCGCCA 300 TACTACTAATCCTTACCCTTATACTACTAGTATTATTCACACCCGACCTACTTGGAGACC 360 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds. ACTICCIATITGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472 Mitochondrial cytochrome b gene sequence SEQ ID NO:39. molecular evidence in forensics BP (COUL) COUNCIL SCI & IND RES 28-MAR-2001; 2001WO-IN000055, 28-MAR-2001; 2001WO-IN000055. ABQ83334 standard; DNA; 472 18-JAN-2003 (first entry) WPI; 2003-018945/01. Verma SK, Singh L; WO200277278-A1 Unidentified. 03-OCT-2002 ABQ83334; 301 301 361 361 421 421 RESULT 8 ABQ83334 ò ద à 셤 à g

Example 1; Page 28-57; 128pp; English.

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The present introduction user. Incept samplifying a fragment of creek AB083297 and AB083299, capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method for the identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal crime in it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the geographical location of the controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the commitment of animal meat in food products for the purpose of food fortification by the order to establish the origin of blood or blood stains collected from the scene of the crime telated to offenses such as murder and rape, in order to establish the origin of blood or blood as murder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the crime investigators and animal at the scene of the crime to confuse the crime investigators and The present invention describes universal primers, mcb 398 and mcb 869

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          converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents a mitochondrial cytochrome b gene sequence from the present invention
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forensic scientists with human blood, and so that the method can be
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                                                                   Sequence 472 BP; 141 A; 148 C; 62 G; 121 T; 0 U; 0 Other;
                                                                                                                        Indels
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                                                                                             79.3%; Score 374.4; DB 8; 87.1%; Pred. No. 6.3e-107; ive 0; Mismatches 61;
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The present invention describes universal primars, man stock of see AB083297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction cytochrome b gene of any animal species in polymerase chain reaction of unknown origin at species and sub-species level. Also described is a coff unit of its used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the rime with the criminal beyond a reasonable doubt, to establish the identity of the purpose of biological materials such as skin, horns confiscated from animal criminal beyond a reasonable doubt, to establish the identity of any so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to detect the confinent of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the confinence of the crime related to offenses such as murder and rape, in order to establish the origin of blood or blood stains collected from the scene of the crime to confine the crime investigators and former animal at the scene of the crime to confine the crime investigators and formed to animal at the scene of the crime to confine the crime investigators and converted to a commercial molecular kit and DNA chips based applications of the crime from the present invention. 360 240 300 120 61 TCCCATATATCGGCACAGACCTGGTCGAATGAATCTGAGGAGGATTCTCCGTAGACAAAG 120 121 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATTCTCCCCTTTATTATCGCTGCCCTTG 180 300 360 420 420 09 9 181 ccaracrecrateracretricrecaecaaaacaecrecaacaaecrecraeaeaarecer CAGACGCAGACAAAATTCCATTCCACCCTACTACACTATCAAAGATATCCTAGGAGCTC 241 CAGACACAGACAAAATCCCATTCCACCTTACTATACCATTAAAGACATCTTAGGCGCCC 301 TACTACTAATTCTAGTCCTCATACTACTATTATTCACACCCGACCTACTTGGAGACC mcb 398 and mcb 869 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGGGGTTCTCAGTAGATAAAG 121 CAACCCTTACCCGATTTTTCGCCTTCGACTTTATCCTCCCATTTATCATTGCAGCCCTTA CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCACAGGAATCTCAT TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 361 cagacaarraraccccagcaaarccacrragcacgcccccccacarcaaaccrgaargar 1 TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCCAACCTTCTCTCAGGAA mitochondrial cytochrome b gene sequence from the present invention 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA Gaps New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for .. 0 ACTICCTATITIGCATACGCAATCCTCCGATCAATTCCTAACAACTAGGAGG Score 372.8; DB 8; Length 472; Pred. No. 2e-106; 0; Mismatches 62; Indels 0 Sequence 472 BP; 139 A; 152 C; 61 G; 120 T; 0 U; 0 Other; invention describes universal primers, 0; Mismatches Example 1; Page 28-57; 128pp; English molecular evidence in forensics. 79.0%; Matches 410; Conservative Query Match Best Local Similarity 301 421 421 181 241 361 셤 셤 ò q à à ద ò 셤 õ d ð ద ò ਨੇ

TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120 rcccarararrcccacaaacrragragaargaarcrgagggarrcrccgragacaaag 120 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA 180 121 CCACCCTCACCCGATTCTTTGCCTTCCATTCTTCTTCTCCCATTCATCATCACCACGCCCTCG 180

61

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300

CAGACACAGAGAAAATCCCATTCCACCCTACTACACAATCAAAGATATCCTAGGCATCG 300

TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC rectactaarcercaccercaractacracretrearececceaceracresses CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT

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241

CAGACGCAGACAAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC

181

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CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCACAGGAATCTCAT

240

360 420 420

ds.

Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene;

Mitochondrial cytochrome b gene sequence SEQ ID NO:16.

18-JAN-2003 (first entry)

BP.

ABQ83311 standard; DNA; 472

RESULT 11 ABQ83311 ABQ83311;

361 CAGACAACTACACTCCAGCAAACCCACTCAACAACCCCCTCACATCAAGCCCGAGTGAT

ACTICCIATITIGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 421 ACTICCTATTIGCATACGCAATCCTACGATCAATCCCCAACAACTAGGCGG

421

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New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.
                                                                                           Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 472 BP; 144 A; 163 C; 60 G; 105 T; 0 U; 0 Other;
                                                                         Mitochondrial cytochrome b gene sequence SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                              Example 1; Page 28-57; 128pp; English.
                   ABQ83330 standard; DNA; 472 BP.
                                                                                                                                                                                                                     (COUL ) COUNCIL SCI & IND RES
                                                                                                                                                                                 28-MAR-2001; 2001WO-IN000055.
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                                                        (first entry)
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                                                                                                                                            WO200277278-A1
                                                                                                                         Unidentified
                                                        18-JAN-2003
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                                                                                                                                                                                                                                        Verma SK,
                                      ABQ83330;
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RESULT 10
           ABQ83330
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The present invention describes universal primers, mcb 398 and mcb 869 (see AB033297 and AB033298), capable of amplifying a fragment of cytochrome begane of any animal species in polymerase chain reaction of (PCR) and revealing the identity of the biological material of any animal cof unknown origin at species and sub-species level. Also described is a certood for the identification of the animal from a biological sample. The criminal beyond a reasonable doubt, to establish the identity of poachers, if it is that of an endangered species for the purpose of controlled, rot have an idea of the geographical location of the court of molecular evidence of animal hunting and related crime in the court of controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene hapolytype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of foot fortification, by the food fortification agencies, to provide a universal from it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal at the scene of the crime to confuse the crime investigators and formal and information in forensics. The present sequence represents and animal didnife indentification in present sequence represents a mitochondrial cytochrome b gene sequence from the present invention

28-MAR-2001; 2001WO-IN000055 28-MAR-2001; 2001WO-IN000055

WO200277278-A1. Unidentified

03-OCT-2002.

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The present invention describes universal primers, mcb 398 and mcb 869 (see AB033297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of
                                                                                                                                                                                                                                                                                                                                                                                                                              New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 28-57; 128pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TACCATGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCCTTTCAGCAA
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Matches 410; Conservative

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Local Similarity

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poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to have an idea of the special primer invented, to detect the pached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food contification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and corensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications of a mitochondrial cytochrome b gene sequence from the present invention
biological materials such as skin, horns confiscated from animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 472 BP; 152 A; 140 C; 57 G; 122 T; 0 U; 1 Other;
   85555555555555555555555
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0; Gaps Length 472; Indels Query Match 78.8%; Score 371.8; DB 8; Best Local Similarity 86.7%; Pred. No. 4.1e-106; Matches 409; Conservative 0; Mismatches 63;

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180 240 CAGACGCAGACAAAATTCCATTCCACCCTACTACACTATCAAAGATATCCTAGGAGCTC 300 300 120 recentacaresecadaarerasresaarsaarerassesessarrereserasaaa 120 CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCCACAGGAATCTCAT 240 121 caaccerracecearririnescrinceacrirarececearriariarearascaaris 180 9 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA 181 CCATAGTTCACCTACTATTCCTCCACGAAACAGGTTCTAACAATCCAACAGGAATTTCCT TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 61 61 121 241 임 ð 임 ò 셤 ò 셤 ð qq ò

301 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC 360 241 CAGACACAGACAAAATTCCATTCCACCCTTACTATACCATTAAAGACATCCTAGGAGGCT 301 TATTACTAATTCTAACTCTAATACTACTAGTACTATTCGCACCGGACCTCCTCGGAGACC CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 361 CAGATAACTACACCCCAGCAAATCCACTTAACACACCTCCCCACATCAAACCGAATGAT 361

421 ACTICITATITICCATANGCAATITIACGGICAATCCCCAACAACTAGGAGG 472 421 ACTICCIATITGCATACGCAATCCICCGAICAATTCCTAACAAACTAGGAGG

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ABQ83313 standard; DNA; 472 RESULT 12 ABQ83313

18-JAN-2003 (first entry)

Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds. Mitochondrial cytochrome b gene sequence SEQ ID NO:18.

Unidentified

The present invention describes universal princip.

(see AB083297 and AB083298) capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal conference of animal butting and related crime in the court of poachers, if it is that of an endangered species, for the purpose of controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the condition of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal confirmation of animal meat in food products for the purpose of food fortification by the origin of blood conformation of animal at the scene of the crime related to offenses such as marder and rape, in order to establish the origin of blood found at the scene of the crime to confuse the crime investigators and conversed to a commercial molecular kit and DNA chips pased applications conversed to a commercial molecular kit and DNA chips based applications conversed to converse the animal at the scene of the crime to converse the converse to a commercial molecular kit and DNA chips based applications. present invention describes universal primers, mcb 398 and mcb 869 converted to a commercial molecular kit and DNA chips based application for wildlife identification in forensics. The present sequence repress a mitochondrial cytochrome b gene sequence from the present invention New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for Sequence 472 BP; 147 A; 145 C; 63 G; 117 T; 0 U; 0 Other; Example 1; Page 28-57; 128pp; English. molecular evidence in forensics (COUL) COUNCIL SCI & IND RES 28-MAR-2001; 2001WO-IN000055 28-MAR-2001; 2001WO-IN000055 WPI; 2003-018945/01. Singh L; WO200277278-A1. 03-OCT-2002 Verma SK,

Gaps ; 0 78.6%; Score 371.2; DB 8; Length 472; 86.7%; Pred. No. 6.4e-106; Indels 63; 0; Mismatches Matches 409; Conservative Best Local Similarity Query Match

1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA

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120 9 1 TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 61 recearacarceacacaaaceragrigaargaarcraagegeegeereereagaagacaaag CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA 121

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241 CAGACGCAGATAAAATCCCATTTCACCCCTACTACACTATTAAAGACATTCTAGGAGCCC 300 CAGACGCAGACAAAATTCCATTCCACCCTACTACACTATCAAAGATATCCTAGGAGCTC 241

420

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301 TACTACTTATTCTAGCCCTAATAATACTAGTACTATTCGCACCCGACCTCCTCGGAGACC 360
                                                         CAGACAACTACACCCCAGCAAACCCACTTAGCACACCTCCCCCATATTAAGCCCGGAATGGT
 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
                                         CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATACACCCCAAATGAT
                                                                                                                                                                                                                                        Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds.
                                                                                                ATTICCTGTTCGCATACGCAATTCTACGATCAATCCCCAACAACTAGGAGG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                             New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for
                                                                                  ACTICCIATITGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472
                                                                                                                                                                                                                       Mitochondrial cytochrome b gene sequence SEQ ID NO:37.
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                                                                                                                                                         ABQ83332 standard; DNA; 472 BP.
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The present invention describes universal primers, mcb 398 and mcb 869 (see AB083297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal for the biological material of any animal cof unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method for the identification of the animal from a biological sample. The criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal correct of an endangered species, for the purpose of biological revidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of confication, by the food fortification agencies, to provide a universal confication, by the food fortification agencies, to provide a universal confication of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime related to found at the scene of the crime related to found at the scene of the crime related to animal at the scene of the crime related to animal at the scene of the crime intentionally spread the blood of animal animal at the scene of the crime to confluse the crime investigators and forensic scientists with human blood, and so that the method can be Example 1; Page 28-57; 128pp; English.

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converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents a mitochondrial cytochrome b gene sequence from the present invention
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                                                                                                                                                                                                                                                                                                       CCATAGTACACCTACTGTTTCTCCCACGAAACAGGATCCCAACAACCCCCACAGGAATCTCAT
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                                                                                                                Gaps
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                                                     Sequence 472 BP; 143 A; 157 C; 59 G; 113 T; 0 U; 0 Other;
                                                                                                             63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrial cytochrome b gene sequence SEQ ID NO:33.
                                                                                Score 371.2; DB 8;
Pred. No. 6.4e-106;
0; Mismatches 63;
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86.7%;
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ABQ83310

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controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to configue the crime investigators and animal at the scene of the crime to configue the crime investigators and
                                                                                                                                                                                                                       (see AB083297 and AB083298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the identity of biological materials such as skin, horns confiscated from animal criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification in forensics. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         converted to a commercial molecular kit and DNA chips based applications for wildlife identification in foreneins may a commercial molecular be and the method applications for wildlife identification in foreneins.
                                                                                                                                                                                                   present invention describes universal primers, mcb 398 and mcb 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a mitochondrial cytochrome b gene sequence from the present invention
fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.
                                                                                                                                          Example 1; Page 28-57; 128pp; English.
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Sequence 472 BP; 143 A; 157 C; 59 G; 113 T; 0 U; 0 Other;

ö 420 120 180 240 240 241 CGGACACAGATAAAATTCCCTTCCACCCTTACTACACCATTAAAGACATCCTAGGTGCCA 300 301 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC 360 360 420 120 121 ccacccreaccearrerrescerreactriarrrecearreareaceaeceres 180 241 CAGACGCAGACAAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC 300 9 60 61 Trccararriggcacaaaccragrcgaargaarcrgaggggggarrcrcagragacaaag CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCACAGGAATCTCAT ccaragrecaceracrerecedegaacagarecaacaacacecedegarecear recraeratereacerearatracraeratracraerecreaceratereceasace CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT CAGACAACTACACCCCAGCAAACCCACTTAACACTCCCCCTCACATCAAACCTGAATGAT 1 TACCATGAGGACAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 1 IACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA Gaps ACTICCTATITICCATACGCAAICTIACGATCACAAICCTAATAAACTAGGAGG 472 421 ACTICCIATITGCAIACGCAAICCICCGAICAAITCCIAACAAACTAGGAGG 472 ,0 Length 472; Indels Query Match 78.6%; Score 371.2; DB 8; Best Local Similarity 86.7%; Pred. No. 6.4e-106; Matches 409; Conservative 0; Mismatches 63; 121 181 181 301 361 361 임 qq 임 à 엄 ò 셤 Š 셤 à g 8 ਨੇ ð

The present invention describes universal primers, mcb 398 and mcb 869 (see ABQ83297 and ABQ83298), capable of amplifying a fragment of youtchinnee b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of goached animal luchtified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime crime. LOT WILDLITE LIGHTILICATION IN forensics. The present sequence represents a mitochondrial cytochrome b gene sequence from the present invention converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be Mitochondrial cytochrome b gene; mitochondrial; cytochrome b; identification; criminal investigation; animal poaching; gene; ds. New universal primers, mcb 398 and mcb 869, capable of amplifying fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for Mitochondrial cytochrome b gene sequence SEQ ID NO:15. Example 1; Page 28-57; 128pp; English. molecular evidence in forensics. ABQ83310 standard; DNA; 472 BP (COUL) COUNCIL SCI & IND RES 28-MAR-2001; 2001WO-IN000055 28-MAR-2001; 2001WO-IN000055. 18-JAN-2003 (first entry) WPI; 2003-018945/01. Singh L; 40200277278-A1 Unidentified. 03-OCT-2002 Verma SK,

61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120 9 9 1 TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 1 TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 78.3%; Score 369.6; DB 8; Length 472; 86.4%; Pred. No. 2e-105; 1.ve 0; Mismatches 64; Indels 0. Sequence 472 BP; 139 A; 157 C; 61 G; 115 T; 0 U; 0 Other; 0; Mismatches Matches 408; Conservative Best Local Similarity Query Match 유 à 8

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RESULT 15

421

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Search completed: November 17, 2004, 00:09:12 Job time: 770.82 secs

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Acaronia Scapanus

AB076816 Scapanus
AB076817 Scapanus
AB122097 Tragulus
AB122099 Tragulus
AB122100 Tragulus
AB122100 Tragulus
AB122101 Tragulus
AB122102 Tragulus
AB122105 Tragulus
AB122107 Tra

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AF123633 327 bp DNA linear VRT 01-MAY-2002 Perissocephalus tricolor cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/db_xref="teaxon:32630"
/note="Universal primer for amplifying a fragment of cytochrome b gene of animal species in polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 6; Length 26; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                    Verma,S.K. and Singh,L.
Universal primers for wildlife identification
Patent: WO 02077278-A 3 03-OCT-2002;
Council of Scientific and Industrial Research (IN)
Location/Qualifiers
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Sequence 3 from Patent WO02077278.
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AY545529
DNJ225116
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MIAACYTBA
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                     AB076816
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AY065721 Hylopezus
AF189111 Cryptoter
AY188015 Dromicodr
AF217828 Aspidelap
AF00931 Archocent
AY333994 Herichthy
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AF123617 Pipreola
AF127194 Grallaria
AF127202 Hylopezus
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AX565571 Sequence
AF376882 Yuhina za
U81343 Chelus fimb
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U86834 Phyllotis w
                                                  November 16, 2004, 22:33:39 ; Search time 142.229 Seconds (without alignments) 8644.709 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                  AX565562 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                          9053458
      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                          4526729 seqs, 23644849745 residues
                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
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AY150649
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AY323994
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AF127202
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AF217828
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AF189111
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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PAT 29-NOV-2002

linear

AY273917 Akodon in AY545529 Cratogeom AJ225116 Dryomys n

AY208610 Pomachrom

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Gaps

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/tb_xref="G1:8050349"
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LVLFLIPFLHKSKQRTWTFRPLSQLMFWALVSNLLILTWVGSQPVEHPFIIIGQLASI
SYFTILLIILFPAIGALENKIINL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondrion Grallaria guatimalensis (scaled antpitta)
Karallaria guatimalensis
Eukaryota; Metazoa; Ocordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-FEB-1999) Ecology and Evolutionary Biology,
University of Kansas, Natural History Museum, Lawrence, KS 66045,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krabbe, N., Agro, D.J., Rice, N.H., Jacome, M., Navarrete, L. a Sornoza, M.F.
Sornoza, M.F.
A new species of antpitta (Formicariidae: Grallaria) from southern Ecuadorian Andes
Auk 116 (4), 882-890 (1999)
2 (bases 1 to 378)
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Sornoza, M.F.
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DEFINITION Hylopezus fulviventris cytochrome b gene, partial cds;
                                                                                                                                                            Length 375;
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/organism="Grallaria_guatimalensis"
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Similarity 100.0%; Score 26; DB 5;
Similarity 100.0%; Pred. No. 1.2;
26; Conservative 0; Mismatcher ^
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'mol type="genomic DNA"
'isolate="Grgu"
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/protein_id="AAF68150.1"
/db_xref="G1:7715713"
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AF127202/c
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AFRELSQFLFWILVANLLILTWIGSQPVEHPFIIIGQLASIAYFTTLLILFFPIIGALE
NKIINL"
                                                                                                            Prum, R.O., Rice, N.H., Mobley, J.A. and Dimmick, W.W.

Prum, R.O., Rice, N.H., Mobley, J.A. and Dimmick, W.W.

A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)

Based on Mitochondrial Dic Hypothesis for the Cotingas (Cotingidae)

Auk 117 (1), 236-241 (2000),

J. Tobases I. To 327) (2000),

Prum, R.O., Rice, N.H., Mobley, J.A. and Dimmick, W.W.

Direct Submission
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Pipreola arcuata cytochrome b gene, partial cd8; mitochondrial gene
AF123617
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1 (bases 1 to 375)
Prum, R.O., Rice, N.H., Mobley, J.A. and Dimmick, W.W.
A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
Based on Mitcohondrial DNA
Auk 117 (1), 236-241 (2000)
2 (bases 1 to 375)
  mitochondrion Perissocephalus tricolor (capuchinbird)
Perissocephalus tricolor
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Avegi Neognathae; Passeriformes; Cotingidae;
Perissocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                        Submitted (26-JAN-1999) Systematics and Ecology, University of Kansas, Natural History Museum, Lawrence, KS 66045, USA Location/Qualifiers
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Direct Submission
Submission
Submitted (26-JAW-1999) Systematics and Ecology, University of
Kansas, Natural History-Museum, Lawrence, KS 66045, USA
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    .327
forganism="Perissocephalus tricolor"
forganel=="mitochondrion"
mol_type="genomic DNA"
db_xref="taxon:114336"

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/codon start=1
/transl_table=2
/product="cytochrome b"
/protein id="AAF71639.1"
/db_xref="G1:8050380"</pre>
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/db_xref="taxon:114366"
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/codon start=1
/transI_table=2
/product="cytochrome b"</pre>
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AF123617/c
                             ORGANISM
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VERSION KEYWORDS SOURCE ORGANISM

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Yuhina zantholeuca cytochrome b gene, partial cds; mitochondrial AF376882
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Archosauria; Aves; Neognathae; Passeriformes; Corvoidea; Corvidae;
                                                                                                                                                                                                                                                                                                                                                                    Sigmoceros lichtensteinii (Lichtenstein's hartebeest)
Sigmoceros lichtensteinii
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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3 (bases 1 to 477)
(bases 1, Kalyakin,M., Han,L.-X. and Pasquet,E.
Direct Submission
Submitted (20-JUN-2002) Ornithology, Museum National d'Histoire Naturelle, 55 rue Buffon, Paris 75005, France Sequence update by submitter
Location/Qualifiers
1. 477
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Cibois, A., Kalyakin, M.V., Han, L.-X. and Pasquet, E.
Molecular phylogenetics of babblers (Timaliidae): revaluation of the genera Yuhina and Stachyris
J. Avian Biol. 33 (4), 380-390 (2002)
Cibois, A., Kalyakin, M., Han, L.-X. and Pasquet, E.
Direct Submission
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    6; Length 472;
                                                                                                                                                                                                                                                        linear
                                             0; Indels
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    .472
    forganism="Sigmoceros lichtensteinii"
/mol type="unassigmed DNA"
/db_xref="taxon:69836"

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100.0%; Score 26; DB 100.0%; Pred. No. 1.2; Live 0; Mismatches
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Sequence 12 from Patent W002077278.
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AX565571.1 GI:26000921
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AF376882/c
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lilflydpflhmskortmtfrplsolmfwilvtnlliltwygsopvehpfiigglasf
tyffillilfptygalenkmlnl"
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                                                                                                              Hylopezus fulviventris
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves; Neognathae, Passeriformes, Formicariidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Alcelaphinae, Alcelaphus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-FEB-1999) Ecology and Evolutionary Biology,
University of Kansas, Natural History Museum, Lawrence, KS 66045,
                                                                                             mitochondrion Hylopezus fulviventris (fulvous-bellied antpitta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                              A new species of antpitta (Formicariidae: Grallaria) from the
                                                                                                                                                                                                                              Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
Sornoza,M.F.
                                                                                                                                                                                                                                                                                                                                                                         Krabbe, N., Agro, D.J., Rice, N.H., Jacome, M., Navarrete, L. and
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       mitochondrial gene for mitochondrial product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hylopezus fulviventris"
/organelle="mitochondrion"
/mol type="genomic DNA"
/isolate="Hyfu"
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/mol_type="unassigned DNA"
/db_xref="taxon:59517"
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Alcelaphus buselaphus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF68157.1"
/db_xref="GI:7715728"
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'product="cytochrome_b"
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Auk 116 (4), 882-890 (1999)
2 (bases 1 to 378)
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/codon start=1
/transl_table=2</pre>
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                                                  AF127202.1 GI:7715727
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Sornoza, M.F.
                                                                                                                                                                                            Hylopezus.
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RESULT 6 AX565570/c

Matches

DEFINITION

LOCUS

SOURCE ORGANISM

KEYWORDS

VERSION

TITLE JOURNAL

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MGYVLDWGQMSFWGATVITNLLSALEYTGHTWYTWIWGRESVDNATLTRFFTLHFWMP
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LFAYAILRSIPNKLGGVLALAASILVLFLMPLLHTSKLRSMTFRPLSQILFWTLVAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AABS7645_1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear VRT 27-FEB-2002 mitochondrial gene encoding
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Tobaes 1 to 892)
Shaffer, H. B., Meylan, P. and McKnight, M. L.
Tests of turtle phylogeny: molecular, morphological, and paleontological approaches
Syst. Biol. 46 (2), 235-268 (1997)
                                                                                                                                                                                                                                                                                                           Gaps
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Submitsation
Submitted (19-DEC-1996) Evolution & Ecology, University of
California, Davis, CA 95616, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                       Length 477;
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organism="Yuhina zantholeuca"
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Chelus fimbriata cytochrome b gene,
mitochondrial protein, partial cds.
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/mol type="genomic DNA"
/db xref="taxon:181641"
                                                                     <1. . . 477
/ codon start=1
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/protein id="AAM46122.1"
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RNLHANGASFFICIYLHIGRGFYYGSYLYKETWNTGVILLLTLMATAFVGYVLPWGQ
MSFWGATVITNLFGAIPYIGQTLVBWAWGGFSVDNPTLTRPFALHFLLPFVIAGLALI
HLTFLHETGSNNPLGISSNCDKIPPHPYFSTKDALGFLLMITPLLTLAMFSPNLLGDP
ENFTPANPLYTPPHIFKPWYFLFAYALLRSIPNKLGGVLALAASVLVLFFSPLLHKSK
QRTWTFRPLSQLLFWALVANLLILTWVA"
                                                                                                                                                    VRT 30-SEP-2003
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Phyllotis wolffsohni
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Willis, E.O.
Affinities of the saw-billed hermit (Ramphodon naevius) determined by cytochrome-b sequence data
Wilson Bull. (2003) In press
2 (bases 1 to 912)
                                                                                                                                                                                                                                                                                                                          Androdon aequatorialis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Trochiliformes, Trochilidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Willis, E.O.
Direct Submission
Submitted (16-SEP-2002) Department of Zoology and the Zoological
Museum, University of Wisconsin, 250 North Mills Street, Madison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene,
partial cds.
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Bleiweiss,R., Hendrickson,S.L., Berres,M.E., Willis,Y.O.
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protein,

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/organism="Androdon aequatorialis"
/organelle="mitochondrion"

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/codon_start=1
/trans1_table=2
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Length 892; 0; Indels

DB 5; 0.96;

100.0%; Score 26; 100.0%; Pred. No.

0; Mismatches

26; Conservative

Similarity

Query Match Best Local

Matches

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Matches 26; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LELAMHYTSDTATAESSYTHICRDVNYGWLIRYMHANGASMFFICMFIHVGRGTYGS
YULSETWNIGIILLITTMATAFVGYYLPWGQMSFWGATVISNLLSAIPYIGXTLVEWI
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            Phylogenetic relationships and species limits within Phyllotis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                    Direct Submission
Submitted (24-July 1997) Laboratory of Molecular Systematics,
Smithsonian Institution, Museum Support Center, 4210 Silver Hill
Road, Suitland, MD 20746, USA
Location/Qualifiers
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Irestedt, M., Fjeldsa, J., Johansson, U.S. and Ericson, P.G.P.
Systematic relationships and biogeography of the tracheophone subcoscines (Aves: Passeriformes)
MMOL. Phylogenet. Evol. 23 (3), 499-512 (2002)
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Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
Direct Submission
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0.95;
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                                                                                                                                                                                                                       /organism="Phyllotis wolffschni"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="MSB 67270"
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/organelle="mitochondrion"
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i; Pred. No. 0.95
0; Mismatches
                                                           J. Mammal. 79 (2), 573-593 (1998), 2 (bases 1 to 929) Steppan, S.J.
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/trans1_table=2
/product="cytochrome_b"
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2 (bases 1 to 999)
Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
Direct Submission
Submitted (05-DEC-2001) Dept. of Vertebrate Zoology, Swedish Museum of Natural History, P.O. Box 50007, Stockholm SE-10405, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY065721 1999 bp DNA linear VRT 15-JUL-2002 Hylopezus fulviventris cytochrome b (cytb) gene, partial cds; mitochondrial gene for mitochondrial product.
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PHIKPEWYFLFAYAILRSIPNKLGGVLALAASVLILFLIPFLHKSKORTMTFRPLSQL
MFWILVVNLLILTWVGSQPVEHPFIIIGQLASLAYFTTLIILFPIIGALENKMLNL"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Formicariidae,
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Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
Systematic relationships and biogeography of the tracheophone suboscines (Aves: Passeriformes)
MOI. Phylogenet. Evol. 23 (3), 499-512 (2002)
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/organelle="mitochondrion"
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VRT 07-JAN-2004

gene, complete

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Nagy, Z.T., Joger, U., Wink, M., Glaw, F. and Vences, M.
Multiple colonization of Madagascar and Socotra by colubrid snakes:
evidence from nuclear and in the phylogenies
Proc. R. Soc. Lond., B. Biol. Sci. 270, 2613-2621 (2003)
2 (Bases I to 1111)
Nagy, Z.T., Joger, U., Wink, M., Glaw, F. and Vences, M.
Direct Submission.
                                                                                                                                                              mitochondrion Dromicodryas quadrilineatus
Dromicodryas quadrilineatus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-NOV-2002) Department of Pharmacy and Molecular Biotechnology, Biological Section, University of Heidelberg, Im Neuchheimer Feld 364, Heidelberg 69120, Germany 3 (bases 1 to 1111) May, F. and Vences, M. Direct Submission Submitted (27-Ocr-2003) Department of Pharmacy and Molecular Biotechnology, Biological Section, University of Heidelberg, Im Neuchheimer Feld 364, Heidelberg 69120, Germany Sequence update by submitter
                        AY188015
Dromicodryas quadrilineatus cytochrome b (cyt b) g cds; mitochondrial gene for mitochondrial product.
                                                                                                                                                                                                                                                             Colubridae, Boodontinae, Dromicodryas.
1 (bases 1 to 1111)
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AY188015.1 GI:37778272
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Kalotermitidae;
Cryptotermitinae; Cryptotermes.

I (bases 1 to 1056)
Thompson, G.J., Miller, L.R., Lenz, M. and Crozier, R.H.
Phylogenetic analysis and trait evolution in Australian lineages of drywood termites (Isoptera, Kalotermitidae)
MGL. Phylogenet.-Bvel--17 (3), 419-429 (2000)
                                                                                                                                                                                                                                                                                                                                                                   Cryptotermes austrinus cytochrome b (Cytb) gene, partial cds; mitochondrial gene for mitochondrial product.
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MFWILVTNLLLITWYGSQPVEHPFIIIGQLASFTYFTILLILFPTVGALENKMLNL"
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    .1056
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/organelle="mitochondrion"

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Pred. No. 0.93;
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Thompson, G.J. and Crozier, R.H.
Direct Submission
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EVWLSGTILLITLMATAFFGYVLPWGQMSFWAATVITNLLTAIPYLGTILTTWLWGGF
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residues to the mRNA"
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Location/Qualifiers
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Nesult Score Match Length DB ID DEBORY NO. Score Match Length DB ID DEBORY 1 286.4 60.7 16569 4 US-09-525-906-1 Seque Seque 60.7 16569 4 US-09-377-866-1 Seque 60.7 16569 4 US-09-377-866-1 Seque 7. 286.4 60.7 16569 4 US-09-377-866-1 Seque 7. 286.4 60.7 16569 4 US-09-377-866-1 Seque 7. 286.4 60.7 16569 4 US-09-377-861-2 Seque 7. 286.4 60.7 16569 4 US-09-377-861-2 Seque 1.95 41.3 614 3 US-09-385-982-185 Seque 6. 195 41.3 614 3 US-09-385-982-185 Seque 6. 13 10.9 5.9 1 US-09-385-982-185 Seque 6. 13 10.9 5.9 1 US-09-386-982-195 Seque 6. 13 10.9 5.9 1 US-09-386-982-11-62 Seque 6. 13 10.9 5.0 1 US-09-386-982-11-62 Seque 6. 13 10.9 5.0 1 US-09-386-111-62 Seque 6. 13 10.9 5.0 1 US-09-386-111-62 Seque 6. 13 10.9 5.0 1 US-09-386-111-62 Seque 6. 13 10.4 21.5 255 4 US-09-736-719 Seque 7. 10.4 21.5 255 4 US-09-288-719 Seque 7. 10.4 21.5 2			₩			SOMMERTES	
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16 127.8 27.1 835 3 US-08-998-416-533 17 127.8 27.1 836 3 US-08-998-416-886 18 101.4 21.5 255 4 US-09-702-705-719 20 101.4 21.5 255 4 US-09-702-719 21 101.4 21.5 255 4 US-09-736-457-719 22 101.4 21.5 255 4 US-09-671-24B-719 23 101.4 21.5 255 4 US-09-681-84-719 24 101.4 21.5 255 4 US-09-681-84-719 25 826 17.5 321 4 US-09-658-824-719 26 17.5 321 4 US-09-678-716-716-716-716-718-718-718-718-718-718-718-718-718-718	Н	127.8	27.1		m	US-08-998-416-1032	1032,
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υ	31	54.6	11.6	1512	4	US-09-252-991A-7793	Sequence 77	7793, Ap
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	33	45.4	9.6	1338	4	US-09-252-991A-7696	Sequence 76	7696, Ap.
O	34	43.4	9.5	740	٣	US-08-998-416-971	Sequence 97	1, App
υ	35	38	8.1	1141	4	US-09-806-708B-22	Sequence 22,	
	36	35.6	7.5	3451	~	US-08-743-637B-18	Sequence 18,	, Appl
	37	35.6	7.5	3451	3	US-08-526-840B-18	Sequence 18	, Appl
	38	33.4	7.1	840	ო	US-09-453-702B-207	Sequence 20	207, App
۲,	39	33.2	7.0	505	4	US-09-621-976-15639	Sequence 15	639, A
r	40	32.8	6.9	289	m	US-09-007-005-17	Sequence 17	7, Appl
υ	41	32.8	6.9	289	m	US-09-244-796-17	Sequence 17	, Appl
r)	42	32.8	6.9	2429	3	US-09-386-493-3	Sequence 3,	3, Appli
υ	43	32.6	6.9	832	4	US-09-621-976-2813	Sequence 28	2813, Ap
υ	44	32.4	6.9	957	4	US-09-248-796A-2649	Sequence 26	2649, Ap
	45	32	6.8	2699	4	US-10-148-689-2	Sequence 2,	Appli

ALIGNMENTS

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15203 TCCCATACATTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCGCTACTCAGTAGACACTC 15262
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75.4%; Pred. No. 5.3e-86;
live 0; Mismatches 116;
                                                                              APPLICANT: Jen, Jen
APPLICANT: Sidransky, David
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Kenneth
APPLICANT: Kinzler, Bert
APPLICANT: Fliss, Makiko
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Mitochondrial Dosimeter
FILE REFERENCE: 1107.85815
CURRENT APPLICATION NUMBER: US/09/525,906
CURRENT APPLICATION NUMBER: 09/377,856
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1999-08-20
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 1, Application US/09525906
Patent No. 6605433
GENERAL INFORMATION:
APPLICANT: Jen, Jen
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Best Local Similarity 75.4
Matches 356; Conservative
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ORGANISM: Homo sapiens
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US-09-525-906-1
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CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCACAGGGAATCTCAT 240
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                                                                                                                                                   TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
                                                                       CAGACGCAGACAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC
                                                                                                         ccarrccdaraaarcaccrrcaccrracracaaarcaaacaarcaaaacccrcacrrac
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Pred. No. 5.3e-86;
0; Mismatches 116; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Markers
FILE REFERENCE: 1107.82346
CURRENT APPLICATION NUMBER: US/09/377,856
CURRENT FILING DATE: 1999-08-20
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FASELSEQ for Mindows Version 3.0
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Patent No. 6344322
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SEQ ID NO 1
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                                               15443 Trcrcrrcrrcrccrraargacarraacacrarrcrcaccacaccacacccrccradgedadd 15502
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                                                                                       CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT
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Sequence 2, Application US/09097889

Sequence 2, Application US/09097889

Setemation 0. 6218110

APPLICANT: Herrnstadt, Corrina

APPLICANT: Ghosh, Soumirra S.

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOC NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 286.4; DB 3; 75.4%; Pred. No. 5.3e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 16569 base pairs TYPE: nucleic acid STRANDEDNESS: single
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Matches 356; Conserv
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TOPOLOGY: lin
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Herrnstadt, Corrina Ghosh, Soumitra S.

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APPLICANT: Clevenger, William
APPLICANT: Faby, Boin F.
APPLICANT: Party, Boin F.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                             STATE: Washington
COUNTRY: USA
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15204 TCCCATACATIGGGACAGACCTAGTICAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15263
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                                                                421 ACTICCIATITGCAIACGCAAICCICCGAICAAITCCIAACAAACIAGGAGG 472
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Glosh, Soumitra S.
APPLICANT: Glosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Rahy, Boin F.
APPLICANT: Rahy, Boin F.
APPLICANT: Pany, Boin F.
APPLICANT: Pany, Boin F.
TITLE OF INVENTION: QUANTIFICATION OF EXTRAMITOCH(FILE OF INVENTION: QUANTIFICATION OF EXTRAMITOCH(FILE OF INVENTION: WIMBER: US/09/302,681
CURRENT APPLICATION NUMBER: US/09/302,681
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FRAESEQ for Windows Version 3.0
SEQ ID NO:
                                                                                                                                                                                                          Sequence 2, Application US/09302681 Patent No. 6441149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 16569
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US-09-302-681-2
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           COMPUTER KEALBLE FORD

COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION NUMBER: GEOBB. J.
RECISTRATION NUMBER: 660088.416
RECISTRATION NUMBER: 660088.416
RECISTRATION NUMBER: 660088.416
TELEPHONE: (206) 682-601
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 286.4; DB 4;
Pred. No. 5.3e-86;
0; Mismatches 116;
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Best Local Similarity 75.4%;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Sequence 2, Application US/09098079 Patent No. 6489095 GENERAL INFORMATION:

RESULT 5 US-09-098-079-2

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TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REPRENCE: COLNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
MUMBER: 0F SEQ ID NOS: 544
SOFTWARE: FASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 284.8; DB 4;
Pred. No. 4.5e-86;
0; Mismatches 117;
APPLICANT: HINO, FUMITSUGU
APPLICANT: KATO, IKUNOSHIN
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
TITLE OF INVENTION: CANCER-ASSOCIATED GENES
CURRENT APPLICATION NUMBER: US/09/377,497
CURRENT FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 70
SOGTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 1140
                                                                                                                                                                                                                                                                                               FEATURE:

COTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-7
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; Sequence 185, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
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ilarity 75.2%;
Conservative 0
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ORGANISM: Homo sapiens
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Matches 355; Conserv
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15564 ATTICCTATICGCCTACACAATTCTCCGATCCGTCCCTAACAAACTAGGAGG 15615
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                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Wogelstein, Bert
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
TITLE OF INVENTION: Warkers
FILE REPERBNCE: 1107.82346
CURRENT APPLICATION NUMBER: US/10/053,611
FILE REPERBNCE: 1107.82346
FRIOR APPLICATION NUMBER: US/09/377,856
PRIOR PRILING DATE: 1999-08-20
FRIOR FILING DATE: 1999-08-20
FRIOR FILING DATE: 1999-08-20
FRIOR FILING DATE: 1999-08-20
SOFTWARE: FRESEE FOR ID NOS: 1
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0; Mismatches 116;
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                                                                                                                    Sequence 1, Application US/10053611
Patent No. 6750021
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APPLICANT: MUKAI, HIROYUKI
APPLICANT: ASADA, KIYOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 356; Conserv
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LENGTH: 16569
                                                                                              US-10-053-611-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: HOUS-10-053-611-1
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US-09-377-497-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GACAGTCCCACCCTCACAGATTCTTTACCTTTCACTTCATCTTGCCCTTCATTATTGCA
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                                                                                                                                                                                                                                                                                                                     Length 614;
                                                                                                                                                                                                                                                                                                                                                                                              95; Indels
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
                                                                                                                                                                                                                                                                                                                     Score 195; DB 3;
Pred. No. 6.9e-56;
0; Mismatches 95;
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CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER PILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASELSE FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 493, Application US/09385982 Patent No. 6262334 GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                   ) NAME/KEY: misc_feature

| LOCATION: (1)...(614)

| CTHER INFORMATION: n = A,T,C or G

US-09-385-982-185
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 73.3%;
Matches 263; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1)...(591)
                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 591
LENGTH: 614
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548 CCNTCACNNGATINTITACCTITCATTTCATCTTGGCCTTCATTAATGCAGCCCTAGCAG 489
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                                                                                                        488 CATICCACTICTATICTIGGGAGGAACGGGATCAACCACCCCCTTAGGAATCACCTCC
                                                                                                                                                                                          243 GACGCAGACAAAATTCCATTCCACCCTACTACACTATCAAAGATATCCTAGGAGCTCTA
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                                                                 184 TAGTACACCTACTGTTTCTC-CACGAAACAGGATCCAAACAACCCCACAGGAATCTCATCA
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REPERENCE: COLONA-Z60X
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-10
EARLIER APPLICATION NUMBER: 00/132,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER PILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTERQ for Windows Version 3.0
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Pred. No. 1.1e-50;
0; Mismatches 137;
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Patent No. 6262334
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; OTHER INFORMATION: n = A,T,C or
US-09-385-982-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1%;
Best Local Similarity 65.8%;
Matches 265; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
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APPLICANT: Steinman, Kathleen E.
APPLICANT: Steinman, Kathleen E.
APPLICANT: Burgess, Christopher C.
APPLICANT: Burgess, Christopher C.
APPLICANT: Burgess, Christopher C.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOWBER: US/09/328,111
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER PILING DATE: 1999-06-08
EARLIER PILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 763
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)...(578); OTHER INFORMATION: n = A,T,C or G US-09-328-111-763
                               GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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US-09-328-111-562/c
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301 ATACCCTAGCCAACCCCTTAAACACCCCTCCCCACATCAAGCCCGAATGATATTTCCTAT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTACCATAGTACACCTAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tritrincificarititatnifice--freatrandadecerageagraniceneric 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 IGTITCTCCACGAAACAGGATCCAACCACCCCACAGGAATCTCATCAGACGCAGACAAAA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTTTGGCACGAAGGGATCAACCAACCCTTAGNAATCACTTCCCATTCNGATAAA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTCTACTATTAATTT-TA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 ACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGGAGACCCCAGACCTATACA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reacutriceacerrianiacaearcaaseacecereaagerriarririrerriere 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 TCNTTAATGACATTAACACTATTCTCACCAGACCTCTTAGGGGGACCCAGACAATTATACC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGATACTTCCTATTTGCA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crasceaaccentraaacaccerceceacarcaaccecaarcaararrrecrarresec 237
                                                                 ATACACCAGGAAACCCACTTAATACACCCCCACATATCAAGCCCGAAATGATACTTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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                                                                                                                                                                             0; Mismatches 105; Indels
                                                                                                                                                       430 ITGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
APPLICANT: WILSON O., ET AL.
APPLICANT: WILSON O., ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACACAATTCTCCGATCCGTCCCTAACAACTAGGAGG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%; Score 149.4; DB 3; 68.0%; Pred. No. 1.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CCUNA-266XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER PELING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FESTSEQ for Windows Version 3.0
EENGTH: 619
                                                                                                                                                                                                                                                                                                     Sequence 510, Application US/09385982
Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature;
LOCATION: (1).T.(619)
CTHER INFORMATION: n = A,T,C or G
US-09-385-982-510
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Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 619
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                   US-09-385-982-510/c
                                                                 370
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268
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                                                                                                                                                                                                                                                                                                                              509 TTANTACACAATCAAAGACGCCCTNGGCTTACTTCTTTCTTCTTCTTCTTAATGACAT 450
                                                                                                                                                                                                                                                                                                                                                                                                   TAGTCCTATTCTCACCGGACCTGCTTGGAGACCCAGACAACTATACACCAGCAAACCCAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 TIAATACACCCCACATATCAAGCCCGAATGATACTTCCTATTTGCATACGCAATCCTCC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 TAAACACCCTCCCCACATCAAGCCCGAATGATATTTCCTATTCGCCTACACAATTCTCC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 TAACACTATTCTCACCAGACCTCNTAGGCGACCCAGACAATTATACCCTAGCCAACCCT 390
                                                                                                                                   209 AACAGGATCCAACCCCACAGGAATCTCATCAGAGGCGGAGACAAAATTCCATTCCACCC
                                                                                                                                                                                              569 AACGCGATCAACCAACCCCTTAGGAATCACTTCCCATTCCGATAAAATCACCTTCCACCC
                                                                     Gaps
                                                                        1;
Query Match 30.9%; Score 146; DB 3; Length 578; Best Local Similarity 74.0%; Pred. No. 2.4e-39; Matches 196; Conservative 0; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 GATCAATTCCTAACAAACTAGGAGG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 562, Application US/09328111; Patent No. 626233
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Rathleen E.
APPLICANT: Astle, Jon H.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll Abnam APPLICANT: Porti, Adnam APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
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RESULT 12 US-09-328-111-763/c ; Sequence 763, Application US/09328111

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RESULT 15
US-08-998-416-1032/c
; Sequence 1032, Application US/08998416
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 GAAAAGGGNNTCAAACAACCCCCTTAGNATCACTTCCCATTCCGGATAAAATCACCTTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCCC-TACTACACTATCAAAGATATCCTAGGAGCT--CTACTATTAATTTTAACCCTC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 caccectráctacacaarcaascaceceresserractreferirentenentes 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 CCACTTTATCCTCCCATTTATCATTGCAGCCCTTACCATAGTACACCTACTGTTTCTCCA
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Patent No. 6239264

GENEAL INFORMATION:
APPLICANT: Poblimann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                               APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER PILING DATE: 1999-06-10
SOFTWARE: FABLESQ for Windows Version 3.0
SECTION OF SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 130.4; DB 3;
Pred. No. 4.5e-34;
0; Mismatches 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(597)

OTHER INFORMATION: n = A,T,C or G
US-09-328-111-562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.6%;
Best Local Similarity 62.8%;
Matches 246; Conservative
   APPLICANT: Monahan, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-998-416-190/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 597
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181 CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCACAGGAATCTCAT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 CTACTATTATAAGATTCTTTCTTTTTCATTTTAGTACCATTTATTATTGCAGCAATAG 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 GTAATTTAGATAGATTACCAATGCATGGTTATTTTTATATAAAGATTTAGTAACAGTAT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 TICCATITATIGGAAAIGAIATIGIACIATGAITATGAGGAICATITAGIGITAGÍAAIC 332
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                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INPORMATION:
NAME: Meigs, J Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 27.1%; Score 127.8; DB 3; Best Local Similarity 55.2%; Pred. No. 3.5e-33; Matches 249; Conservative 0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ACTICCIATITGCATACGCAATCCTCCGATC 451
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o. 6239264th Carolina
USA
                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CAGACGCAGACAAAATTCCATTCCACCCCTACTACTATCAAAGGTATCCTAGGAGCTC 300
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                                                                                            ...rutCANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No Corress:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.1%; Score 127.8; DB 3; Length 716; 55.2%; Pred. No. 3.7e-33; ive 0; Mismatches 202; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 6239264artis Corporation
STREBT: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 249; Conserv
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Search completed: November 17, 2004, 03:15:13 Job time : 169.862 secs

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(without alignments)
3621.431 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USIO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3625171 segs, 2700493622 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                           nucleic search, using
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472
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	% Query Match	* Query Match Length DB	DB	ΩI	Description	
	318.4	67.5	16300	19	US-10-191-803-11	Sequence 11, Appl	
1 73	315.2	66.8		16	US-10-191-803-2	Sequence 2, Appli	
m	311	62.9	416	0	US-09-960-352-12545	Sequence 12545, A	
4	308.2	65.3	411	σ	US-09-960-352-3407	Sequence 3407, Ap	
Ŋ	308	65.3	412	0	US-09-960-352-9822	Sequence 9822, Ap	
9	301.6	63.9		σ	US-09-960-352-8757	8757,	
7	288	61.0		16	US-10-308-264-370	Sequence 370, App	
80	288	61.0	16569	16	US-10-308-264-479		
6	288	61.0		16	US-10-308-264-213		
10	288	61.0		16	US-10-308-264-287	Sequence 287, App	
11	286.4	60.7		16	US-10-308-264-150	Sequence 150, App	
12	286.4	60.7		16	US-10-308-264-214	Sequence 214, App	

21, App	App	App	App	App	App	App	App	App	App	App	App	App	ppli	App	App	App	pli	ppli	ppli	App1	App	App	App	App	App	App	App	App	App	App	App1	Appl
221,	373,	206,	264,	180,	420,	168,	448,	198,	199,	204,	326,	376,	1, A	367,	548,	ഥ	-:	Н	_	М	477,	480,	495,	499,	502,	510,	516,	526,	527,	531,	10,	10,
Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence		Sequence 2	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

Query Match 67.5%; Score 318.4; DB 16; Length 16300; Best Local Similarity 79.7%; Pred. No. 1.2e-88; N

us-09-821-782e-48.rnpb

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Bos taurus
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Best Local Similarity
Matches 350; Conserv
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OTHER INFORMATION:
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US-09-960-352-12545
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US-09-960-352-12545
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LENGTH: 416
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Publication No. US20040014040A1

GENERAL INFORMATION:

APPLICANT: MENDRICK, Donna

APPLICANT: MORTER, Mark

APPLICANT: JOHNSON, Kory

APPLICANT: HGGS, Brandon

APPLICANT: HGGS, Brandon

APPLICANT: GASTLE, Arthur

APPLICANT: GASTLE, Arthur

APPLICANT: GASTLE, Arthur

TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

FILE REFERENCE: 2002-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2002-06-03

PRIOR FILING DATE: 2002-06-06

NUMBER OF SEQ ID MOS: 1140

SOSTWARE: PATENTIN VET: 2.1
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US-10-191-803-2
   96; Indels
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Pred. No. 4.5e-88;
0; Mismatches 98;
   Mismatches
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79.2%;
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ORGANISM: Rattus norvegicus
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Best Local Similarity 79.2
Matches 374; Conservative
376; Conservative
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TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA

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Sequence 12545, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Mathialagan, Magappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: US/0298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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llarity 84.1%; Pred. No. 4.7e-87;
Conservative 0; Mismatches 66
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Sequence 8757, Application US/09960352
Patent No. US20020137139A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, NaCLE ADD END OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPRESENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengling
APPLICANT: Tao, Nengling
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
ITILE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
ITILE OF INVENTION: MUSCLE AND FAI DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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361 AACTACACCCCAGCCAATCCACTCAACACACGGA
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OTHER INFORMATION; Clone ID: 42-LIB34-012-Q1-E1-C10
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                                                                                                                                Sequence 9822, Application US/09960352 Patent No. US20020137139A1
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US-09-960-352-8757
                                                                                                             US-09-960-352-9822
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 9822
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nugappan
TITLE OF INVENTION: NUCLBIC ACLD AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MGG/37-21(10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 3407
LENGTH: 411
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                                                                                                                                       241 GGGCCCTCTTACTAATTCTAGCTCTAATACTACTAGTACTATTGGCACCCGACCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unsure at all n locations
Clone ID: 15-LIB34-003-Q1-E1-D11
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3407, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Bos taurus FEATURE:
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LOCATION: (289)

OTHER INFORMATION: u

CTHER INFORMATION: C

US-09-960-352-3407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "n" refers to a nucleotide at position 3107 of the Cambridge Reference Sequence (CRS, Anderson et al. 1981 Nature 290:457-465), later determined to be absent from the human mcDNN sequence according to the revised CRS (rCRS, Andrews et al. 1999 Nature Genetics 23:147); "n" therefore represents a single nucleotide deletion at a position corresponding nucleotide 3107 of SRQ ID NO:1 as provided herein.
                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                   69 ATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAGCAACCCTT
                                                                                                                                                                                                                                                     1 ATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGAAAGCAACCCTT
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llarity 75.6%; Pred. No. 4.1e-79;
Conservative 0; Mismatches 115; Indels 0;
                                                                                                                                                 Length 448;
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                                                                                                                                              63.9%; Score 301.6; DB 9; Length 84.2%; Pred. No. 4.4e-84; ive 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG
                                                                   ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Herrnstadt, Corinna
TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
FILE REFERENCE: 660089.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
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NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                           Best_Local Similarity 04.2
Matches 340; Conservative
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US-10-308-264-370
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LENGTH: 16565
<211> conflict
TYPE: DNA
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                    SEQ ID NO 8757
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                                                        TYPE: DNA
                                                                                                                                              Query Match
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                                   LENGTH:
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Best_Local Similarity Matches 357; Conserv

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15438 TICICITCCTICTCCTTAATGACATTAACACTATTCTCACCAGACCTCCTAGGCGACC 15497
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                                                     15138 recegigadecaaararearicidadeeecaeaeraaraaaerracaaerraeearee
                                                                                                                                                                            15198 TCCCATACATTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15257
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TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTTCAGCAA
                                                                                                                                                                                                                                       121 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA
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                                                                                                                                                                                                                                                                                                                                                           181 CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACACCCCACAGGAATCTCAT
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Pred. No. 4.1e-79;
0; Mismatches 115; Indels 0;
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Sequence 479, Application US/10308264

Publication No. US20040029133A1

GENERAL INFORMATION:

APPLICANT: Herrnstadt, Corinna

TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMOI

FILE REFERENCE: 660088.461

CURRENT PILING DATE: 2002-11-25

NUMBER OF SEQ ID NOS: 697

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 479
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ORGANISM: Homo sapiens mitochondrial
FEATURE:
LOCATION:
OTHER INFORMATION: "n" refers to a nucl
OTHER INFORMATION: Cambridge Reference
OTHER INFORMATION: 1981 Nature 290:457-
OTHER INFORMATION: Absent from the huma
OTHER INFORMATION: Absent from the huma
OTHER INFORMATION: Senetics 23:147, "n
OTHER INFORMATION: Single nucleotide
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Best Local Similarity 75.6%;
Matches 357; Conservative (
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<211> conflict
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REATURE:

CREANIEWH Homo sapiens mitochondrial

FEATURE:

LOCATION: 3110

CTHER INFORMATION: Un" refers to a nucleotide at position 3107 of the OTHER INFORMATION: 1981 Nature 20:457-465), later determined to be OTHER INFORMATION: absent from the human mtDNA sequence according to OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature OTHER INFORMATION: senelica 23:147); "" therefore represents a OTHER INFORMATION: single nucleotide deletion at a position corresponding to OTHER INFORMATION: uncleotide deletion at a position corresponding to OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15267 ccacccrcacacatrcritaccritcatriraccritcatricatratracacccrac 15326
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61.0%; Score 288; DB 16; Length 16572;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0;
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Publication No. US20040029133A1
GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corinna
TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
FILE REFERENCE: 660088.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT PILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
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TYPE: DNA
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10CATION: 3107 of the
10CATION: 3107 of the
10CATION: 3108 "n" refers to a nucleotide at position 3107 of the
10THER INPORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
10THER INFORMATION: 1981 Nature 290:457-465), later determined to be
10THER INFORMATION: absent from the human mtDNA sequence according to
10THER INFORMATION: the revised CRS (LCRS, Andrews et al. 1999 Nature
10THER INFORMATION: Genetics 23:147); "n" therefore represents a
10THER INFORMATION: single nucleotide deletion at a position corresponding to
10THER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
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              15204 TCCCATACATTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15263
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Fublication No. US20040029133A1
GENERAL INFORMATION:
TILLS OF INVENTION:
FILLE REFERENCE: 660088.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILLING DATE: 2002-11-25
CURRENT FILLING DATE: 2002-11-25
SOFTWARE FRASEQ for Windows Version 4.0
SEQ ID NO 213
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<211> conflict
TYPE: DNA
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DNA POLYMORPHISM
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TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMO;
FILE REFERENCE: 660088.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 214
LENGTH: 16559
                                                                                                                                           Sequence 214, Application US/10308264 Publication No. US20040029133A1 GENERAL INFORMATION:
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Best Local Similarity 75.44
Matches 356; Conservative
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                              Trcrcrrcrrcrandacarnaacachticrcacagachchagegac
                                                                                                5507 CAGACAATTATACCCTAGCCAACCCCTTAAACACCCCTCCCCACATCAAGCCCGAATGAT
TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
                                                                   CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGGAATGAT
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                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM FILE REFERENCE: 660088.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING 2002-11-25
NUMBER OF SEQ ID NOS: 697
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens mitochondrial
                                                                                                                                                                                                                                                              ; Sequence 150, Application US/10308264; Publication No. US20040029133A1; GENERAL INFORMATION:
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les 356; Conserv
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 150
LENGTH: 16559
<211> conflict
TYPE: DNA
                                                                                                                                                                                                                           RESULT 11
US-10-308-264-150
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TYPE: DNA
ORGANISM: Homo sapiens mitochondrial
FRATURE:
CCATION: 3106
OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
OTHER INFORMATION: Cambridge Reference Sequence (REA, Anderson et al.
OTHER INFORMATION: absent from the human mtDNA sequence according to
OTHER INFORMATION: absent from the human mtDNA sequence according to
OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
OTHER INFORMATION: single nucleotide deletion at a position corresponding to
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15554 ATTICCIATICGCCTACACTACTCCCGATCCGTCCCTAACAAACTAGGAGG 15605
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Pred. No. 1.3e-78;
0; Mismatches 116; Indels 0;
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TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
FILE REFERENCE: 660088.461
                                                                          APPLICANT: Herrnstadt, Corinna
TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
FILE REFERENCE: 660088.461.
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 221
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                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens mitochondrial
             Sequence 221, Application US/10308264 Publication No. US20040029133A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            FEATURE:
10CATION: 3106
OTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION: 1
OTHER INFORMATION: 2
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OTHER INFORMATION: 5
OTHER INFORMATION: 5
OTHER INFORMATION: 5
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<211> conflict
TYPE: DNA
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US-10-308-264-373
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US-10-308-264-221
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LOCATION: 3107

OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al. OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be OTHER INFORMATION: absent from the human mtDNA sequence according to OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature OTHER INFORMATION: Genetics 23:147); "n" therefore represents a OTHER INFORMATION: single nucleotide deletion at a position corresponding to OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
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Pred. No. 1.3e-78;
0; Mismatches 116; Indels 0;
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TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
FILE REFERENCE: 660088.461
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
SOFTWARE: FASTSEQ for Mindows Version 4.0
CURRENT APPLICATION NUMBER: US/10/308,264
CURRENT FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 697
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 373
LENGTH: 16560
<211>CONFILES CONFLICE
TYPE: DNA
                                                                                                                                                                                                                                                ORGANISM: Homo sapiens mitochondrial
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75.4%;
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Best Local Similarity 75.4<sup>§</sup>
Matches 356; Conservative
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LENGTH: 16561
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                                                   "n" refers to a nucleotide at position 3107 of the Cambridge Reference Sequence (CRS, Anderson et al. 1981 Nature 290:457-465), later determined to be absent from the human mcDNA sequence according to the revised CRS (rCRS, Andrews et al. 1999 Nature Genetics 23:147); "n" therefore represents a single nucleotide deletion at a position corresponding nucleotide 3107 of SEQ ID NO:1 as provided herein.
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ORGANISM: Homo sapiens mitochondrial
FEATURE:
LOCATION: 3108
OTHER INFORMATION: "n" refers to a nucl)
OTHER INFORMATION: Cambridge Reference
OTHER INFORMATION: 1981 Nature 220:457-70.
OTHER INFORMATION: the revised CRS (rCF)
OTHER INFORMATION: Genetics 23:147); "r
OTHER INFORMATION: single nucleotide dd;
OTHER INFORMATION: nucleotide 3107 of SUS-10-308-264-206
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ILTGLFLAMHYTADTTTAFSSVTHICRDVNYGWIIRYMHANGASMFFICLFMHVGRGI
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VEWINGGFSVDKATLTRFFAFHFILPFIIAALTHVHLLFHETGSNNPTGISSDADKI
PFHPYYTIKDILGGALLLILTLAMLIVESPDLLGDPDNYTPANPLNTPPHIKPEWYFLF
AYAILKSIPNKLGGVLALVLSILILLIMPMLHTSKQQSMMFRRISQCLFWVLVADLLL
LTWIGGQPVEHPYIIIGQLASVMYFLLILVLMPVASTIENNLLKW"
                                                                                                                                                                                                                                                                                                                                                                    AF022058
Antilope cervicapra cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matthee, C.A. and Robinson, T.J.
Cytochrome b phylogeny of the family bovidae: resolution within the alcelaphini, antilopini, neotragini, and tragelaphini
Mol. Phylogenet. Evol. 12 (1), 31-46 (1999)
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Antilope cervicapra
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Antilopinae; Antilope.
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Submitted (02-SEP-1997) Zoology & Entomology, University of
Pretoria, Lynnwood Street, Pretoria, Gauteng 0002, South Africa
Location/Qualifiers
                CAGACAACTATACACCCAGCAAACCCCACTTAATACACCCCCACATATCAAGCCCGAATGAT
                                                             CAGACGCAGACAAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC
CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACACCCCACAGGAATCTCAT
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Matthee, C.A.
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AF022058
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AF036283 1139 bp DNA linear MAM 01-DEC-1999
Antilope cervicapra cytochrome b (cytb) gene, mitochondrial gene
encoding mitochondrial protein, partial cds.
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Submitted (02-DEC-1997) Systematique Moleculaire (GDR 1005), Museum
National d'Histoire Naturelle, 43, rue Cuvier, Paris 75005, France
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                          458 TCCCATACATCGGTACAAAACCTAGTAGAATGAATCTGAGGGGGGTTCTCAGTAGAAG
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1 (Bases 1 to 1139)

Hassanin, A. and Douzery, E.J.

The tribal radiation of the family Bovidae (Artiodactyla)

Wolution of the mitochondrial cytochrome b gene

Mol. Phylogenet. Evol. 13 (2), 227-243 (1999)
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     Indels
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/organelle="micochondrion"
/mol type="genomic DNA"
/db_xref="taxon:59525"
  0; Mismatches
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CF64528 CEGO8735
CN822842 Oa. splbn.
BG689885 338199 BA.
CR49349 703541 MA.
CR44300 695671 MA.
CR44500 695671 MA.
CR44500 695671 MA.
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BM43529 1Ru1587.a
BM43623 1RR11A03
CN89904 4124424 B.
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CN89904 4124424 B.
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CR536710 771751 MA.
CR536710 171773 MA.
CR536710 171703 MA.
BM434031 1RT01B01
                                                                                                                       November 16, 2004, 22:24:28; Search time 6487.97 Seconds (without alignments) 2650.992 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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25 335.8 22 23 335.8 22 23 337.8 23 331.2 2 3331.2 2 3331.2 2 3331.2 2 3331.2 2 3331.2 2 334 3331.2 2 328.8 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	RESULT 1 CN822665 LOCUS LOCUS DEFINITION OA SPLDIN aries cDM ACCESSION CN822665 VERSION CN822665 VERSION CN822665 SOURCE OVIS arie ORGANISM OVIS arie ENTRES AUTHORS GOSSNET,A TITLE OVINE SPL TOURNAL UNPUBLISH COMMENT Veterinar Universit SUMMENT UNiversit SUMMENT UNiversit SUMMENT UNiversit SOURCE SOURCE SOURCE High qual Hig

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CMG22842 840 bp mRNA linear EST 02-JUN-2004 oa splbn 02G06_Ml3reverse Sheep spleen\brain pSportl library Ovis aries cDNA clone Oa_splbn_02G06 5', mRNA sequence.
                                                                                                               93 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGGTTCTCAGTAGACAAAG 152
                                                                                                                                                                                                  CAACCCITACCCGAITTITCGCCTICCACTITAICCTCCCATITAICAITGCAGCCCTTA 180
                                                                                                                                                                                                                          213 CCATAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAGACAACAGGAATTTCCT 272
                                                                                                                                                                                                                                                                                                                                                                       CAGACGCAGACAAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC 300
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                          33 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCTTATCAGCAA
                             TACCATGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA
                                                                                                                                                                                                                                                                                    CCATAGIACACCTACTGITICTCCACGAAACAGGATCCAACAACACCCACAGGAATCTCAT
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/mol_type="mxNN,"
/db_xref="taxon,"
/clone="Oa_splbn_02606"
/clone_lib="Sheep_spleen\brain_pSport1_library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 ACTTCTATTTGCATACGCAATCTTACGATCACAACAACAAAAACTAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.7%; Score 362; DB 7; Length 840; 86.1%; Pred. No. 2.3e-95; Live 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: J Hopkins
Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 02 row: G column: 06
Seg primer: Ml3reverse
High quality sequence start: 5
High quality sequence stop: 549.
Location/Qualifiers
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1 (bases 1 to 840)
Gossner, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: j.hopkins@ed.ac.uk
Plate: 02 row: G column
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Matches 401; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
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CN822842
LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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JOURNAL
COMMENT
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f\note="\graphygan: skeletal muscle; Vector: Uni-ZAPXR; Site_l:
EcoEl; Site_2: Xho I; Library made from skeletal muscle of
a 14 month old Angus steer."
                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                         446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 670)
Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S., Dierens, L. and Lehnert, S.
                    CTACCCTCACCGGATTTTTCGCCTTTCACTTTATTTTCCCATTCATCATCGAGCCCTCG 266
                                                                                                                                                                                                CAACCCITACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA 180
                                                                                                                                                                                                                                                            TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC 360
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Queensland
                                                                                                           CCATAGTTCACCTACCTCCTCCACGAAACAGGATCCAACAACCCCACAGGAATTCCAT
                                                                                                                                                                                                                                                                                    CAGACAACTACACCCCAGCAAACCCCACTTAACACTCCCCCCTCACAACCTGAATGAT
                                                                                  CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACAACCACAGGAATCTCAT
                                                                                                                                                                         CAGACGCAGACAAAATTCCATTCCACCCTACTACTACTATCAAAGATATCCTAGGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CESSO08735 Bos taurus muscle cDNA library Bos taurus cDNA clone CECLO08735 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Contact: Dr Sigrid Lehnert
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Bioscience Precinct, University of 1306 Carmody Road St.Lucia QLD Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 362.2; DB 7; Length 670; 85.4%; Pred. No. 1.9e-95; tive 0; Mismatches 69; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Longissimus dorsi muscle"
/dev_stage="Young Adult"
/lab_host="XLI-BlueMRF'strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sigrid.Lehnert@csiro.au
11 row: C column: 03.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:9913"
clone="CCL008735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Angus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 07 3214 2445
Fax: 07 3214 2480
Email: Sigrid.Lehr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .670
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Matches 403; Conserv
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SOURCE ORGANISM

REFERENCE

AUTHORS

TITLE

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                                                                                                                                           Query Match
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Matches 40
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AUTHORS
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CB220822
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 571)
Sonsteadd, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E. B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
                                                                                                                                                                                                                                                                              615 CGGACACAGATAAAATTCCCTTCCACCCTTATTACACCATTAAAGACATCCTAGGTGCTA
                     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA
                                                                                                                                                                                                           TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG
                                                                                          rrccararregeacaaaaccragregaargaarcregeaggarrereagragacaaag
                                                                                                                            CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA
                                                                                                                                                                                          CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCACAGGAATCTCAT
                                                                                                                                                                                                                                                                                                                                                                                      CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCCACATATCAAGCCCGAATGAT
TACCATGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTICCTATITGCGTACGAATCTTACGATCAATCCCTAATAAACT 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 ACTICCIATITGCATACGCAATCCTCCGATCCAATTCCTAACAAACT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Bos taurus gene index Mamm. Genome 13 (7), 373-379 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338199 BARC 5BOV BOS taurus CDNA
BG689885
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Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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1. .571
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BG689885
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/clone lib="BARC SBOV"
/note="Vector: pCMV SPORT6, Site_1: Not1; Site_2: Sal1;
Inbrary made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 571;
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                                                                                                                                                                                                                                                                . 69
                                                                                                                                                                                                                Score 361.6; DB 4
Pred. No. 2.8e-95;
0; Mismatches 69
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Insert Length: 574 Std Error: 0.00
POLYA=No.
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:28291336
                                                                                                                                                                                                                76.6%;
85.4%;
                                                                                                                                                                                                                                                                403; Conservative
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Bos taurus
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329. cow: L column: 22
Seq primer: GTAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovinae, Bos.
1 (bases 1 to 727)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
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Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 CAGACGTAGACAAAATCCCATTCCACCTACTATACCATTAAGGACATCTTAGGGGCCC
                                                                                                                                                                                                                          /organism="Bos taurus"
/mol_type="mRNA"
/db xref="taxon:9913"
/tisue_type="pooled"
/lab host="DH108"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/inbrary made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATCATTGCAGCCCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGCTCATCACCAACCTCTTATCAGCAA
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Pred. No. 2.9e-95;
0; Mismatches 69;
                                                                                                                                                                           Location/Qualifiers
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Best Local Similarity 85.4%;
Matches 403; Conservative (
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Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                                                                                                                                                                                  1. .692
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A second set of bovine ESTs from pooled-tissue normalized libraries Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                 /tissue_type="Smooth muscle"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF'-strain"
/clone_lib="Bos taurus Abomasum #1 library"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1:
I; Site_2: Xho I"
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703541 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                            76.6%; Score 361.6; DB 6
85.4%; Pred. No. 2.8e-95;
ive 0; Mismatches 69
                                                          taurus"
                                                     'organism="Bos taurus"
'mol_type="mRNA"
'db_xref="taxon:9913"
Location/Qualifiers
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A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovídae,
                                                                                                 Chitko-McKown, C.G.
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Pred. No. 3e-95;
0; Mismatches 69; Indels
                                                                                             Echternkamp, S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
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                                                              1 (bases 1 to 728)
Smith, T.P.L., Roberts, A.J.,
Wray, J.E. and Keele, J.W.
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                                                                  VSDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Bmail: smith@email.marc.usda.gov
Single pass sequencing: Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
Plate: FQX8052 row: H column: 9
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Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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/db_xref="taxon:9913"
/db_xref="taxon:9913"
/tisaue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/note="vector: pcDNA3.1; Site 1: EcoRI; site 2: NotI;
/incle="vector: pcDNA3.1; Site 1: EcoRI; site 2: NotI;
/incle="vector: pcDNA3.1; Site 1: EcoRI; site 2: NotI;
/including liver. lung, hypothalamus, pituitary, and
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Pred. No. 3e-95;
0; Mismatches 69;
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85.4%;
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403; Conservative
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                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Ovis.
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/db_xref="taxon:940"
/dbone="do splbn 07C24"
/clone_lib="Sheep spleen\brain pSport1 library"
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aries cDNA clone Oa_splbn_07C24 5', mRNA sequence.
CN824188
CN824188.1 GI:47952257
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                                                                                                                                                                                                                                                                                                                                                                                                                76.1%; Score 359; DB 7;
86.0%; Pred. No. 1.8e-94;
ive 0; Mismatches 65;
                                                                                                                                                                        Contact: J Hopkins
Veterinary Blomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
                                                                                                                                                                                                                                      Plate: 07 row: C column: 24
Seg primer: Ml3reverse
High quality sequence start: 6
High quality sequence stop: 550.
                                                                                                                 1 (bases 1 to 863)
Gossnar, A. and Hopkins, J.
Ovine spleen\brain cDNA library
Unpublished (2004)
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/organism≈"Ovis aries"
                                                    Ovis aries (sheep)
Ovis aries
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Best Local Similarity 86.0
Matches 398; Conservative
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CB223436 515 bp mRNA linear EST 10-FEB-2003 1JEJ23E10 Bos taurus Jejunum #1 library Bos taurus cDNA, mRNA sequence.

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                                                                                                                                                                                                  Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M. K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laborators
Dept of AFNS, University of Alberta
Ho Agriffor, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Fax: 780 492 0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGACGCAGACAAAATTCCATTCCACCCTACTACATATCAAAGATATCCTAGGAGCTC 300
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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Site_1: EcoRI; Site_2: Xho I"
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85.2%; Pred. No. 1.6e-93;
tive 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: stephen.moore@ualberta.ca
Insert Length: 515 Std Error: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
GI:28293950
                                                                                                                                                                             (bases 1 to 515)
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Matches 397; Conservative
                                                  (COM)
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                                                                                                                                                        Bovinae; Bos.
                                                  Bos taurus
                                                                             Bos taurus
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Funding for EST sequencing was provided by an INRA funding for EST sequencing was provided by an INRA funding for the CDNA library construction was provided by an EEC contract (BO14-CT95-0190).

The library was constructed by I. Hue, BDR, INRA, 78350

JOUY-EN-JOSAS. The double stranded cDNA was un-directionally cloned in a TA cloning vector. Deal is a SMART cDNA library. Insert size was between 450 and 3500 bp. Sequencing was done from the 5' end of
                                                                                                                                                                 EST 02-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 ACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAGCAACCC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 735)
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//note="Vector: pCR2.1 (Invitrogen); Clone distribution :
AGENBE Resource centre. Francois PIUMI.
Prancois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.733"
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/dev stage="embryon"
/lab_host="DHS"
                                                                                                                                                                 CR451416 CR451416 Day 14 bovine embryos (bcai) Bos taurus cDNA clone
bcai0012a.h.09 5', mRNA sequence.
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  466
                                               552
                      507 ACTICITATITIGCATACGCAAICTTACGAICAATCCCCAACAAACT
421 ACTICCIATITGCATACGCAATCCTCCGATCAATTCCTAACAAACT
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Biologie du Developpement et Reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                Renard, J.P., Sreenan, J.P. and Hue, I. Embryonic ESTs (bcai) Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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/organism="Bos taurus"
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Best Local Similarity 85.2%;
Matches 397; Conservative (
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Bos taurus (cow)
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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                                                                                                                         RESULT 12
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Bos taurus Abomasum #1 library Bos taurus cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                           Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M. K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract Gene Expression Profiling of the Bovine Gastrointestinal Tract Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of ARNS, University of Alberta
410 Agrifor, Dept of ARNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Fax: 780 492 4265
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Smooth muscle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: stephen.moore@ualberta.ca
Insert Length: 552 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Bos taurus"
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CB220605.1 GI:28291119
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Query Match
Best Local Similarity 85.0%;
Matches 397; Conservative
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                   240
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                                             CAGACAAAATTCCATTCCACCCTACTACACTATCAAAGATATCCTAGGAGCTCTACTAT 306
                                                                          241 Tagacaaaarcccarriccacccracrarraccarraaggacarcraagggcccrcrrac 300
                                                                                                          TAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACCCAGACA 366
                                                                                                                                                                    ACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGATACTTCC 426
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/lab_host="DH10B TonA"
/clone_lib="BARC BBOV"
/note="Organ Intestine; Vector: pCMVSport6.1; Site_1:
Not1; Site_2: BcoR1; Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 648)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and
Matukumalli, L.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
301 TAATICTAGCICTAATACTACTAGTACTATICGCACCCCGACCTCCTCGGAGACCCAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                421 TATTTGCATACGCAATCTTACGATCAATCCCCAACAACTAGGAGG 466
                                                                                                                                                                                                                               TATITIGCATACGCAATCCTCCGATCAATTCCTAACAAACTAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9913"
/clone="8BOV_35C22"
/sex="Female"
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Bos taurus
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1 (bases 1 to 560)

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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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#1 library Bos taurus CDNA, mRNA
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/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
Score 355; DB 7; Length 648;
Pred. No. 2.5e-93;
0; Mismatches 70; Indels
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Insert Length: 560 Std Error:
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/organism="Bos
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Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agrif, For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169
Fax: 780 492 4265
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
/clone_lib="Bos taurus Rumen #1 library"
/note="Organ: Rumen; Vector: Uni-2ZAPXR; Site_1: EcoRI;
Site_2: Xho I"
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                                                                                   Length
                                                                                                                     Indels
                                                                                                                       69
                                                                                       DB 4;
                                                                                  Score 354.6; DB 4
Pred. No. 3.2e-93;
0; Mismatches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: stephen.moore@ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM434623.
BM434623.1 GI:18456345
                                                                                       75.1%;
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Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 487
                                                                                       Query Match
Best Local Similarity 85.2
Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taurus
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Bos 1
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BM434623
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ORGANISM
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JOURNAL
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                                                       ORIGIN
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                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGGGGGTTCTCAGTAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                      24 TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCTTATCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATAGTACACCTACTGTTTCTCCACGAAACAGGATCCAACAACCCCCACAGGAATCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT
                                                                                                                                                                                                                                                                                                                                         TACCATGAGGACAAATATCTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 TACTATTAATTTTAACCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                   #1 library"
Uni-2ZAPXR; Site_1:
                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                            487;
/db_xref="taxon:9913"
/tissue_type="fanoth muscle"
/cell_type="fanoth muscle"
/cell_type="Stratified squamous epithelial"
/dev_stage="Young adult"
/lab_host="XiJ-BlueWRF'strain"
/clone_lib="Bos_taurus Reticulum #1 library"
/note="Organ: Reticulum; Vector: Uni-2ZAPARR
BCORI; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ACTICCIATITGCATACGCAATCCTCCGATCAATTCCTAACAAA 464
                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                            Score 353.6; DB 4;
Pred. No. 6.1e-93;
0; Mismatches 69;
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                                                                                                                                                                                                                                            74.9%;
ilarity 85.1%;
Conservative
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